NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TRANSCRIPTION IN PLANTS

This application claims priority under 35 U.S.C §120 of applications No. 09/474,435 filed December 28, 1999, 09/654,617 filed September 5, 2000, No. 09,684,016 filed October 10, 2000, No. 09/733,089 filed 12/11/00, No. 09/620,392 filed July 19, 2000, all of which are herein incorporated by reference in their entirety.

INCORPORATION OF SEQUENCE LISTING

Two copies of the sequence listing (Seq. Listing Copy 1 and Seq. Listing Copy 2) and a computer-readable form of the sequence listing, all on CD-ROMs, each containing the file named pa_00309G.txt, which is 45,480,235 bytes (measured in MS-DOS) and was created on March 22, 2001, are herein incorporated by reference.

FIELD OF THE INVENTION

The present invention is in the field of plant molecular biology. More specifically, this invention pertains to nucleic acid fragments encoding transcription factors, transcription factors, antibodies to transcription factors as well as plants and other organisms expressing transcription factors. This invention also relates to methods of using such agents, for example, in plant breeding.

BACKGROUND OF THE INVENTION

Transcription is the essential first step in the conversion of the genetic information in the DNA into protein and the major point at which gene expression is controlled. Transcription of protein-coding genes is accomplished by the multisubunit enzyme RNA polymerase II and an ensemble of ancillary proteins called transcription factors. Basal (or general) transcription factors (a universal set of cellular proteins required for the transcription of all protein-coding genes) assist RNA polymerase II in aligning itself to the core region encompassing the transcription initiation site of genes and accurately initiating transcription. RNA polymerase II, basal transcription factors and an array of other proteins known as transcription co-factors comprise the basal transcription machinery that determines the constitutive level of gene transcription. Other transcription factors, termed gene-specific transcription factors, modulate transcription of a subset of protein-coding genes in

response to specific environmental signals through binding to characteristic, cis-acting DNA sequence elements (motifs) and interactions with the basal transcription machinery. Cis-acting DNA sequence elements are often parts of larger regulatory entities called promoters or enhancers which confer a specific expression pattern to linked transcription units, their target genes. Collectively, these regions might bind several different gene-specific transcription factors each of which might contribute positively (activators) or negatively (repressors) to transcription initiation and rate. Protein-protein interactions between DNA-bound gene-specific transcription factors often result in synergistic or inhibitory regulatory effects. It is the sum of these combinatorial interactions that defines the transcriptional identity of a gene, turning genes on and off as appropriate for a specific biological context. In this manner, genes can be regulated, for example, tissue specifically, with a certain temporal or developmental pattern or become responsive to exogenous cues.

The identification of transcription factors and the subsequent modification of their activity may result in dramatic changes to a plant leading to plants with highly desirable, commercial traits. Root growth, tolerance to salt or cold stress, and flower characteristics are only some examples of plant traits which may be altered by modifying transcription factors.

Transcription factors may be identified by the presence of conserved functional domains. Typically, they are comprised of two domains that represent discrete functional entities. One of these is responsible for sequence-specific DNA recognition and binding (DNA binding domain); and the other facilitates communication with the basal transcription machinery, resulting in either the activation or repression of transcription initiation (transeffector domain). In addition, transcription factors also may contain oligomerization domains. This domain type may be adjacent to or overlap DNA binding domains and may act with them to effect the transcription factor's affinity for certain cis elements or other aspects of transcription factor activity. Nuclear localization signals which are characterized by a core peptide enriched in arginine and lysine may be present as well.

Such functional domains may be identified by examining the primary amino acid sequence of a putative transcription factor. For example, one class of transcription

factors, the leucine zipper proteins, derive their name from the repeats they share of four or five leucine residues precisely seven amino acids apart. These domains provide hydrophobic faces through which leucine zipper proteins interact to form dimers. Zinc finger proteins are transcription factors so called because of the presence of repeated motifs of cysteine and histidine that are reported to fold up into a three-dimensional structure coordinated by a zinc ion.

Protein domains indicative of transcription factors have been described using Profile Hidden Markov Models (*e.g.* Profile HMM). Profile HMMs are based on position specific sequence information from multiple alignments. Different residues in a functional sequence are subject to different selective pressures. Multiple alignments of a sequence family reveal this in their pattern of conservation. Some positions are more conserved than others, and some regions of a multiple alignment are reported to tolerate insertions and deletions more than other regions.

An HMM (Hidden Markov Model) is used to statistically describe a protein family's consensus sequence. This statistical description can be used for sensitive and selective database searching. The model consists of a linear sequence of nodes with a "begin" state and an "end" state. A typical model can contain hundreds of nodes. Each node between the beginning and end state corresponds to a column in a multiple alignment. Each node in an HMM has a match state, an insert state, and a delete state with position-specific probabilities for transitioning into each of these states from the previous state. In addition to a transition probability, the match state also has position specific probabilities for emitting a particular residue. Likewise, the insert state has probabilities for inserting a residue at the position given by the node. There is also a chance that no residue is associated with a node. That probability is indicated by the probability of transitioning to the delete state. Both transition and emission probabilities can be generated from a multiple alignment of a family of sequences. An HMM can be aligned with a new sequence to determine the probability that the sequence belongs to the modeled family. The most probable path through the HMM (*i.e.* which transitions were taken and which residues were emitted at match and insert sites) taken to generate a sequence similar to the new sequence determines the similarity score.

Several available software packages implement profile HMMs or HMM-like models. These include SAM (cse.ucsc.edu/research/compbio/sam.html), HMMER (pfam.wustl.edu/) and HMMpro (www.netid.com/). Additionally, two collections of profile HMMs are currently available: the Pfam database (pfam.wustl.edu/) and the PROSITE Profiles database (expasy.proteome.org.au/prosite/).

Sequence similarity searches against known transcription factors or transcription factor domains resulting in statistically significant similarity between a putative and known transcription factor also provide strong evidence that both code for proteins with similar three dimensional structure and are thus likely to exhibit equivalent biochemical functions. The use of amino acid comparison methods-in particular those such as BLAST ((Altschul *et al., J. Mol. Biol. 215:*403-410 (1990)) and FASTA (Pearson, W.R. and Lipman, D.J. *Proc. Natl. Acad. Sci. 85*, 2444-2448 (1988)) which are sufficiently fast to search protein sequence databases (such as NCBI's non-redundant amino acid databases, (www.ncbi.nlm.nih.gov or Transfac which contains transcription factor domains (Wingender, E., *et al., Nucleic Acids Res. 28*, 316-319 (2000)) have been used for such purposes. More rigorous algorithms such as that of the Frame+ program (Compugen, www.cgen.com modeled on an algorithm designed by GCG Genetics Computer Group, Madison, WI) are also used.

Nucleic acid sequences and/or translations of nucleic acid sequences disclosed herein are cDNA and genomic sequences which have been queried for the presence of transcription factor functional domains. These sequences may be used in DNA constructs useful for imparting unique genetic properties into transgenic organisms. They may also be used to identify other transcription factor sequences.

SUMMARY OF THE INVENTION

The present invention includes and provides a substantially purified nucleic acid molecule comprising a nucleic acid sequence selected from SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof or fragment of either.

The present invention further substantially provides a purified maize transcription factor, soybean transcription factor, rice transcription factor, *Arabidopsis* transcription

factor and fragment of any encoded by a first nucleic acid sequence which specifically hybridizes to a second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID 13478.

The present invention also provides a substantially purified protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241, and SEQ ID NO: 13479 through SEQ ID NO: 24143 and fragment of any.

The present invention also provides a substantially purified protein or fragment thereof encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478.

The present invention further provides a purified antibody or fragment thereof which is capable of specifically binding to a protein or fragment thereof, wherein the protein or fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; (B) a structural nucleic acid molecule encoding a protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143 and fragment of any; and (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to (B) a transcribed nucleic acid molecule with a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule encoding a protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NO: SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143 and fragment of any; which is linked to (C) a 3' non-translated sequence that functions in plant cells to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a method for determining a level or pattern of a plant transcription factor in a plant cell or plant tissue comprising: (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, the marker nucleic acid molecule selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having the nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 and complements thereof or fragments of any, with a complementary nucleic acid molecule obtained from the plant cell or plant tissue, wherein nucleic acid hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue permits the detection of an mRNA for the transcription factor; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant cell or plant tissue; and (C) detecting the level or pattern of the complementary nucleic acid, wherein the detection of the complementary nucleic acid is predictive of the level or pattern of the plant transcription factor.

The present invention provides a method of determining a mutation in a plant whose presence is predictive of a mutation affecting a level or pattern of a protein comprising the steps: (A) incubating, under conditions permitting nucleic acid hybridization,

a marker nucleic acid, the marker nucleic acid selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having a nucleic acid sequence selected from the group of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof and a complementary nucleic acid molecule obtained from the plant, wherein nucleic acid hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant permits the detection of a polymorphism whose presence is predictive of a mutation affecting the level or pattern of the protein in the plant; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant; and (C) detecting the presence of the polymorphism, wherein the detection of the polymorphism is predictive of the mutation.

The present invention also provides a method of producing a plant containing an overexpressed protein comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region comprises a nucleic acid sequence encoding an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241, SEQ ID NO: 13479 through SEQ ID NO: 24143 and fragment thereof wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in overexpression of the protein; and (B) growing the transformed plant.

The present invention also provides a method of producing a plant containing reduced levels of a plant transcription factor comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region comprises a nucleic acid molecule encoding an amino acid sequence consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292

through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241, SEQ ID NO: 13479 through SEQ ID NO: 24143 and fragment thereof; wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in co-suppression of the plant transcription factor; and (B) growing the transformed plant.

The present invention also provides a method for preventing expression of a plant transcription factor in a plant cell comprising: (A) transforming the plant cell with a knockout construct, said construct comprising a nucleic acid molecule selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof or fragment of either.

The present invention also provides a method for detecting an insertion event in a genome comprising: (A) preparing a DNA composition enhanced for a plurality of insertion junctions; (B) preparing at least a first detectable array comprising said DNA composition, wherein said preparing comprises directly or indirectly attaching said DNA composition to a solid support; (C) hybridizing a gene specific probe to said array, said gene specific probe detecting said insertion event from said first array and said gene specific probe comprising a nucleic acid sequence selected from SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof or fragment of either.

The present invention also provides a method for selecting a plant having a trait, said method comprising the steps of: (A) obtaining genomic DNA from a plurality of plants; (B) analyzing genomic DNA from each of the plurality of plants to determine the presence or absence of a DNA marker that is genetically linked to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof or fragment of either and (C) selecting said plant containing said DNA marker.

The present invention also provides a method for reducing expression of a plant transcription factor in a plant comprising: (A) transforming the plant with a nucleic acid molecule, the nucleic acid molecule having an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule, wherein the exogenous promoter region is linked to a transcribed nucleic acid molecule having a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule having a nucleic acid sequence that encodes a plant transcription factor having an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143 or fragments thereof and the transcribed strand is complementary to an endogenous mRNA molecule; and wherein the transcribed nucleic acid molecule is linked to a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and (B) growing the transformed plant.

The present invention also provides a method of determining an association between a polymorphism and a plant trait comprising: (A) hybridizing a nucleic acid molecule specific for the polymorphism to genetic material of a plant, wherein the nucleic acid molecule has a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID 13478 and complements thereof or fragment of any; and (B) calculating the degree of association between the polymorphism and the plant trait.

The present invention also provides a method of isolating a nucleic acid that encodes a plant transcription factor or fragment thereof comprising: (A) incubating under conditions permitting nucleic acid hybridization, a first nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: through SEQ ID 13478 and complements thereof or fragment of any with a complementary second nucleic acid molecule obtained from a plant cell or

plant tissue; (B) permitting hybridization between the first nucleic acid molecule and the second nucleic acid molecule obtained from the plant cell or plant tissue; and (C) isolating the second nucleic acid molecule.

The present invention also provides an array comprising at least 30 different and separated target nucleic acid molecules immobilized on a solid support in a manner that complementary probe nucleic acid molecules can be hybridized thereto, wherein said target nucleic acid molecules have at least 20 consecutive nucleotides in a sequence selected from the group consisting of: (a) SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143; (b) sequences which are complements of (a); (c) sequences which have at least 60% identity to a sequence of (a) or (b); (d) sequences of molecules which hybridize to a sequence of (a) or (b) or (c).

DETAILED DESCRIPTION OF THE INVENTION

Agents of the Present Invention

Agents

One skilled in the art can refer to general reference texts for detailed descriptions of known techniques discussed herein or equivalent techniques. These texts include *Current Protocols in Molecular Biology* Ausubel *et al.*, eds., John Wiley & Sons, N. Y. (1989), and supplements through September (1998), *Molecular Cloning, A Laboratory Manual*, Sambrook *et al*, 2nd Ed., Cold Spring Harbor Press, Cold Spring Harbor, New York (1989), *Genome Analysis: A Laboratory Manual 1: Analyzing DNA*, Birren *et al.*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1997); *Genome Analysis: A Laboratory Manual 2: Detecting Genes*, Birren *et al.*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1998); *Genome Analysis: A Laboratory Manual 3: Cloning Systems*, Birren *et al.*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1999); *Genome Analysis: A Laboratory Manual 4: Mapping Genomes*, Birren *et al.*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1999); Plant Molecular Biology: A Laboratory Manual, Clark, Springer-Verlag, Berlin, (1997), *Methods in Plant Molecular Biology*, Maliga *et al.*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1995).

These texts can, of course, also be referred to in making or using an aspect of the invention. It is understood that any of the agents of the invention can be substantially purified and/or be biologically active and/or recombinant.

The agents of the invention will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic and thus involve the capacity of the agent to mediate a chemical reaction or response. The term "substantially purified", as used herein, refers to a molecule separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state.

The agents of the present invention may also be recombinant. As used herein, the term recombinant, refers to a) molecules that are constructed outside of living cells by joining natural or synthetic DNA segments to DNA molecules that can replicate in a living cell or b) molecules that result from the replication or expression of those molecules described above.

It is understood that the agents of the invention may be labeled with reagents that facilitate detection of the agent (*e.g.* fluorescent labels, Prober *et al.*, *Science 238*:336-340 (1987)); Albarella *et al.*, EP 144914; chemical labels, Sheldon *et al.*, United States Patent 4,582,789; Albarella *et al.*, U.S. Patent 4,563,417; modified bases, Miyoshi *et al.*, EP 119448). It is further understood that the invention provides recombinant bacterial, mammalian, microbial, archaebacterial, insect, fungal, algal, and plant cells as well as viral constructs comprising the agents of the invention.

(a) Nucleic Acid Molecules

Agents of the present invention include plant nucleic acid molecules and more preferably include maize, soybean, rice and *Arabidopsis thaliana* nucleic acid molecules

and more preferably include nucleic acid molecules of the maize genotypes B73 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), B73 x Mo17 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), DK604 (Dekalb Genetics, Dekalb, Illinois U.S.A.), H99 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), RX601 (Asgrow Seed Company, Des Moines, Iowa), Mo17 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.), and soybean types Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa), C1944 (United States Department of Agriculture (USDA) Soybean Germplasm Collection, Urbana, Illinois U.S.A.), Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), FT108 (Monsoy, Brazil), Hartwig (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), BW211S Null (Tohoku University, Morioka, Japan), PI507354 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), Asgrow A4922 (Asgrow Seed Company, Des Moines, Iowa U.S.A.), PI227687 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.), PI229358 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and Asgrow A3237 (Asgrow Seed Company, Des Moines, Iowa U.S.A.), and rice types, *Oryza sativa* L (japonica type), and more preferably *Oryza sativa* L (japonica type), *cv.* Nipponbare.

Fragment nucleic acid molecules may encode significant portion(s) of, or indeed most of, these nucleic acid molecules. For example, a fragment nucleic acid molecule can encode a rice, maize, soybean or *Arabidopsis* protein or fragment thereof. Alternatively, the fragments may comprise smaller oligonucleotides (having from about 15 to about 400 nucleotide residues, and more preferably, about 15 to about 30 nucleotide residues, or about 50 to about 100 nucleotide residues, or about 100 to about 200 nucleotide residues, or about 200 to about 400 nucleotide residues, or about 275 to about 350 nucleotide residues).

A fragment of one or more of the nucleic acid molecules of the invention may be a probe and specifically a PCR probe. A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (www.genome.wi.mit.edu/

cgi-bin/www-STS_Pipeline), or GeneUp (Pesole *et al.*, *BioTechniques* 25:112-123 (1998)), for example, can be used to identify potential PCR primers.

A particularly preferred embodiment of the nucleic acid molecules of the present invention are plant nucleic acid molecules that comprise a nucleic acid sequence which encodes an *Arabidopsis* transcription factor from one of the categories of transcription factors in Table 1 or fragment thereof, more preferably a nucleic acid molecule comprising a nucleic acid selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO: 3290 or a nucleic acid molecule comprising a nucleic acid sequence which encodes a transcription factor from one of the categories of transcription factors in Table 1 or fragment thereof comprising an amino acid selected from the group consisting of SEQ ID: NO: 1 through SEQ ID NO: 1286.

Another particularly preferred embodiment of the nucleic acid molecules of the present invention are plant nucleic acid molecules that comprise a nucleic acid sequence which encodes a maize transcription factor from one of the categories of transcription factors in Table 1 or fragment thereof, more preferably a nucleic acid molecule comprising a nucleic acid selected from the group consisting of SEQ ID NO: 5479 through SEQ ID NO: 8350 or a nucleic acid molecule comprising a nucleic acid sequence which encodes a transcription factor from one of the categories of transcription factors in Table 1 or fragment thereof comprising an amino acid selected from the group consisting of SEQ ID: NO: 3292 through SEQ ID NO: 5478.

A further, particularly preferred embodiment of the nucleic acid molecules of the present invention are plant nucleic acid molecules that comprise a nucleic acid sequence which encodes a rice transcription factor from one of the categories of transcription factors in Table 1 or fragment thereof, more preferably a nucleic acid molecule comprising a nucleic acid selected from the group consisting of SEQ ID NO: 9242 through SEQ ID NO: 10474 or a nucleic acid molecule comprising a nucleic acid sequence which encodes a transcription factor from one of the categories of transcription factors in Table 1 or fragment thereof comprising an amino acid selected from the group consisting of SEQ ID: NO: 8351 through SEQ ID NO: 9241.

An additional, particularly preferred embodiment of the nucleic acid molecules of the present invention are plant nucleic acid molecules that comprise a nucleic acid sequence which encodes a soy transcription factor from one of the categories of transcription factors in Table 1 or fragment thereof, more preferably a nucleic acid molecule comprising a nucleic acid selected from the group consisting of SEQ ID NO: 10475 through SEQ ID NO: 13478 or a nucleic acid molecule comprising a nucleic acid sequence which encodes a transcription factor from one of the categories of transcription factors in Table 1 or fragment thereof comprising an amino acid selected from the group consisting of SEQ ID: NO: 13479 through SEQ ID NO: 15686.

Nucleic acid molecules or fragments thereof of the present invention are capable of specifically hybridizing to other nucleic acid molecules under certain circumstances. Nucleic acid molecules of the present invention include those that specifically hybridize to nucleic acid molecules having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: SEQ ID 13478 or complements thereof.

Nucleic acid molecules or fragments thereof of the present invention are capable of specifically hybridizing to other nucleic acid molecules under certain circumstances. Nucleic acid molecules of the present invention include those that specifically hybridize to nucleic acid molecules having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291 and SEQ ID NO: 5479 through SEQ ID NO: 8350 and SEQ ID NO: 9242 through SEQ ID NO: SEQ ID 13478 or complements thereof.

As used herein, two nucleic acid molecules are said to be capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure.

A nucleic acid molecule is said to be the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules are said to exhibit "complete complementarity" when every nucleotide of one of the molecules is complementary to a nucleotide of the other. Two molecules are said to be "minimally

complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are said to be "complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook *et al.*, *Molecular Cloning*, A Laboratory Manual, 2nd Ed., Cold Spring Harbor Press, Cold Spring Harbor, New York (1989) and by Haymes *et al.*, *Nucleic Acid Hybridization, A Practical Approach*, IRL Press, Washington, DC (1985). Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. Thus, in order for a nucleic acid molecule to serve as a primer or probe it need only be sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 X sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 X SSC at 50°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 X SSC at 50°C to a high stringency of about 0.2 X SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

In a preferred embodiment, a nucleic acid of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 1287 through SEQ ID NO:3291 and SEQ ID NO: 5479 through SEQ ID NO: 8350 and SEQ ID NO: 9242 through SEQ ID NO: SEQ ID 13478 or complements thereof under moderately stringent conditions, for example at about 2.0 X SSC and about 65°C.

In a particularly preferred embodiment, a nucleic acid of the present invention will include those nucleic acid molecules that specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 1287 through SEQ ID NO:3291 and SEQ ID NO: 5479 through SEQ ID NO: 8350 and SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof under high stringency conditions such as 0.2 X SSC and about 65°C.

In one aspect of the present invention, the nucleic acid molecules of the present invention have one or more of the nucleic acid sequences set forth in SEQ ID NO: 1287 through SEQ ID NO:3291 and SEQ ID NO: 5479 through SEQ ID NO: 8350 and SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof. In another aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 90% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1287 through SEQ ID NO:3291 and SEQ ID NO: 5479 through SEQ ID NO: 8350 and SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof. In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 95% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1287 through SEQ ID NO:3291 and SEQ ID NO: 5479 through SEQ ID NO: 8350 and SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof. In a more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 98% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1287 through SEQ ID NO:3291 and SEQ ID NO: 5479 through SEQ ID NO: 8350 and SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof. In an even more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 99% sequence identity with one or more of the sequences set forth in SEQ ID NO: 1287 through SEQ ID NO:3291 and SEQ ID NO: 5479 through SEQ ID NO: 8350 and SEQ ID NO: 9242 through SEQ ID NO: SEQ ID 13478 or complements thereof.

As used herein "sequence identity" refers to the extent to which two optimally aligned polynucleotide or peptide sequences are invariant throughout the alignment of

nucleotides or amino acids. An "identity fraction" for aligned segments of a test sequence and a reference sequence is the number of identical nucleotides or amino acid residues which are shared by the two aligned sequences divided by the length of the alignment. "Percent identity" is the identity fraction X 100.

Useful methods for determining sequence identity are disclosed in *Guide to Huge Computers*, Martin J. Bishop, *ed.*, Academic Press, San Diego, (1994). More particularly, preferred computer programs for determining sequence identity include the Basic Local Alignment Search Tool (BLAST) programs which are publicly available from National Center Biotechnology Information (NCBI) at the National Library of Medicine, National Institute of Health, Bethesda, Md. 20894; see BLAST Manual, Altschul *et al.*, NCBI, NLM, NIH; Altschul *et al.*, *J. Mol. Biol. 215*:403-410 (1990). Version 2.0 or higher of BLAST programs allow the introduction of gaps (deletions and insertions) into alignments.

Nucleic acid molecules of the present invention also include homologues. Particularly preferred homologues are selected from the group consisting of alfalfa, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, peanut, pepper, potato, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, and *Phaseolus*.

In a preferred embodiment, nucleic acid molecules having SEQ ID NO: 1287 through SEQ ID NO:3291 and SEQ ID NO: 5479 through SEQ ID NO: 8350 and SEQ ID NO: 9242 through SEQ ID 13478 or complements thereof and fragments of either can be utilized to obtain such homologues.

(b) Nucleic Acid Molecules Encoding Proteins or Fragments Thereof

Nucleic acid molecules of the present invention can comprise sequences that encode a transcription factor or fragment thereof. Such transcription factors or fragments thereof include homologues of known transcription factors in other organisms.

In a preferred embodiment of the present invention, a maize, soybean, *Arabidopsis thaliana* or rice transcription factor or fragment thereof of the present invention is a homologue of another plant transcription factor.

In another preferred embodiment of the present invention, a maize, soybean, *Arabidopsis thaliana* or rice transcription factor or fragment thereof of the present invention is a homologue of a fungal transcription factor.

In another preferred embodiment of the present invention, a maize, soybean, rice or *Arabidopsis thaliana* transcription factor of the present invention is a homologue of mammalian transcription factor.

In another preferred embodiment of the present invention, a maize, soybean, rice or *Arabidopsis thaliana* transcription factor or fragment thereof of the present invention is a homologue of a bacterial transcription factor.

In another preferred embodiment of the present invention, a soybean, rice or *Arabidopsis thaliana* transcription factor or fragment thereof of the present invention is a homologue of a maize transcription factor.

In another preferred embodiment of the present invention, a maize, rice or *Arabidopsis thaliana* transcription factor homologue or fragment thereof of the present invention is a homologue of a soybean transcription factor.

In another preferred embodiment of the present invention, a maize, soybean, or *Arabidopsis thaliana* transcription factor homologue or fragment thereof of the present invention is a homologue of a rice transcription factor.

In another preferred embodiment of the present invention, a maize, soybean or rice transcription factor homologue or fragment thereof of the present invention is a homologue of an *Arabidopsis thaliana* transcription factor.

In a preferred embodiment of the present invention, the nucleic molecule of the present invention encodes a maize, soybean, rice or *Arabidopsis thaliana* transcription factor or fragment thereof where a maize, soybean, rice or *Arabidopsis thaliana* transcription factor exhibits a BLAST E value score of less than 1E-08 using default parameters with BLAST version 2.0, preferably a BLAST E value score of between about 1E-30 and about 1E-08 using default parameters with BLAST version 2.0, even more preferably a BLAST probability E value score of less than 1E-30 with its homologue using default parameters with BLAST version 2.0.

In another preferred embodiment of the present invention, the nucleic acid molecule encoding a maize, soybean, rice or *Arabidopsis thaliana* transcription factor or fragment thereof exhibits an E value score with a profile HMM using HMMER software version 2.1.1 with default parameters derived from a transcription factor family of less than 1E1.

In a preferred embodiment of the present invention, the nucleic acid molecule of the present invention encodes a maize, soybean, rice or *Arabidopsis thaliana* transcription factor or fragment thereof where a maize, soybean, rice or *Arabidopsis thaliana* transcription factor exhibits a probability score using a Framealign search using Gencore software version 4.5.4 (Compugen, www.cgen.com) of less than 1E-3 using default parameters.

In a preferred embodiment, nucleic acid molecules having SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements and fragments of either can be utilized to obtain such homologues.

In another further aspect of the present invention, nucleic acid molecules of the present invention can comprise sequences, which differ from those encoding a protein or fragment thereof in SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID 13478 due to fact that the different nucleic acid sequence encodes a protein having one or more conservative amino acid changes. It is understood that codons capable of coding for such conservative amino acid substitutions are known in the art.

It is well known in the art that one or more amino acids in a native sequence can be substituted with another amino acid(s), the charge and polarity of which are similar to that of the native amino acid, *i.e.*, a conservative amino acid substitution, resulting in a silent change. Conserved substitutes for an amino acid within the native polypeptide sequence can be selected from other members of the class to which the naturally occurring amino acid belongs. Amino acids can be divided into the following four groups: (1) acidic amino acids, (2) basic amino acids, (3) neutral polar amino acids, and (4) neutral nonpolar amino acids. Representative amino acids within these various groups include, but are not limited to, (1) acidic (negatively charged) amino acids such as

aspartic acid and glutamic acid; (2) basic (positively charged) amino acids such as arginine, histidine, and lysine; (3) neutral polar amino acids such as glycine, serine, threonine, cysteine, cystine, tyrosine, asparagine, and glutamine; and (4) neutral nonpolar (hydrophobic) amino acids such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine.

Conservative amino acid changes within the native polypeptide sequence can be made by substituting one amino acid within one of these groups with another amino acid within the same group. Biologically functional equivalents of the proteins or fragments thereof of the present invention can have ten or fewer conservative amino acid changes, more preferably seven or fewer conservative amino acid changes, and most preferably five or fewer conservative amino acid changes. The encoding nucleotide sequence will thus have corresponding base substitutions, permitting it to encode biologically functional equivalent forms of the proteins or fragments of the present invention.

It is understood that certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Because it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence and, of course, its underlying DNA coding sequence and, nevertheless, obtain a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the peptide sequences of the proteins or fragments of the present invention, or corresponding DNA sequences that encode said peptides, without appreciable loss of their biological utility or activity. It is understood that codons capable of coding for such amino acid changes are known in the art.

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte and Doolittle, *J. Mol. Biol. 157*, 105-132 (1982)). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines

the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like.

Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, *J. Mol. Biol. 157*, 105-132 (1982)); these are isoleucine (+4.5), valine (+4.2), leucine (+3.8), phenylalanine (+2.8), cysteine/cystine (+2.5), methionine (+1.9), alanine (+1.8), glycine (-0.4), threonine (-0.7), serine (-0.8), tryptophan (-0.9), tyrosine (-1.3), proline (-1.6), histidine (-3.2), glutamate (-3.5), glutamine (-3.5), aspartate (-3.5), asparagine (-3.5), lysine (-3.9), and arginine (-4.5).

In making such changes, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those which are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101 states that the greatest local average hydrophilicity of a protein, as govern by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a protein or fragment thereof set forth in SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or fragment thereof due to the fact that one or more codons encoding an amino acid has been substituted for a codon that encodes a nonessential substitution of the amino acid originally encoded.

Agents of the invention include nucleic acid molecules that encode at least about a contiguous 10 amino acid region of a protein of the present invention, more preferably at least about a contiguous 25, 40, 50, 100, or 125 amino acid region of a protein of the present invention. In a preferred embodiment the protein is selected from the group consisting of a plant, more preferably a maize, soybean, *Arabidopsis* or rice from a transcription factor listed from the group consisting of Table 1.

Agents of the present invention include nucleic acid molecules that encode a maize, soybean, rice or *Arabidopsis thaliana* transcription factor or fragment thereof and particularly substantially purified nucleic acid molecules selected from the group consisting of a Table 1.

Non-limiting examples of such nucleic acid molecules of the present invention are nucleic acid molecules comprising: SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or fragment thereof that encode for a plant transcription factor or fragment thereof.

(c) Protein and Peptide Molecules

A preferred class of agents includes proteins or fragments thereof or peptide molecules having an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 15686. An additional preferred class of proteins are those having an amino acid sequence selected from the group consisting of SEQ ID NO: 15687 through SEQ ID NO: 24143.

As used herein, the term "protein molecule" or "peptide molecule" includes any molecule that comprises five or more amino acids. It is well known in the art that proteins may undergo modification, including post-translational modifications, such as, but not limited to, disulfide bond formation, glycosylation, phosphorylation, or oligomerization. Thus, as used herein, the term "protein molecule" or "peptide molecule" includes any protein molecule that is modified by any biological or non-biological process. The terms "amino acid" and "amino acids" refer to all naturally occurring L-amino acids. This definition is meant to include norleucine, norvaline, ornithine, homocysteine, and homoserine.

One or more of the protein or fragment of peptide molecules may be produced via chemical synthesis, or more preferably, by expressing in a suitable bacterial or eukaryotic host. Suitable methods for expression are described by Sambrook *et al.*, In: *Molecular Cloning, A Laboratory Manual, 2nd Edition, Cold Spring Harbor Press*, Cold Spring Harbor, New York (1989), or similar texts.

A "protein fragment" is a peptide or polypeptide molecule whose amino acid sequence comprises a subset of the amino acid sequence of that protein. A protein or fragment thereof that comprises one or more additional peptide regions not derived from that protein is a "fusion" protein. Such molecules may be derivatized to contain carbohydrate or other moieties (such as keyhole limpet hemocyanin, etc.). Fusion protein or peptide molecules of the invention are preferably produced via recombinant means.

Another class of agents comprise protein or peptide molecules or fragments or fusions thereof comprising SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 15686 and SEQ ID NO: 15687 through SEQ ID NO: 24143 or fragment thereof or encoded by SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 in which conservative, non-essential or non-relevant amino acid residues have been added, replaced or deleted. Computerized means for designing modifications in protein structure are known in the art (Dahiyat and Mayo, *Science* 278:82-87 (1997)).

In a preferred embodiment, nucleic acid molecules having SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements and fragments of any can be utilized to obtain such homologues.

Agents of the invention include proteins comprising at least about a contiguous 10 amino acid region more preferably comprising at least a contiguous 25, 40, 50, 75 or 125 amino acid region of a protein or fragment thereof of the present invention. In another preferred embodiment, the proteins of the present invention include a between about 10 and about 25 contiguous amino acid region, more preferably between about 20 and about 50 contiguous amino acid region and even more preferably between about 40 and about 80 contiguous amino acid region.

In a preferred embodiment the protein is selected from the group consisting of a plant, more preferably a maize, soybean, rice or *Arabidopsis* transcription factor from the group consisting of Table 1. In another preferred embodiment, the protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ

ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 15686 and SEQ ID NO: 15687 through SEQ ID NO: 24143.

Protein molecules of the present invention include homologues of proteins or fragments thereof comprising a protein sequence selected from SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 15686 and SEQ ID NO: 15687 through SEQ ID NO: 24143 or fragment thereof or encoded by SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or fragments thereof. Preferred protein molecules of the invention include homologues of proteins or fragments having an amino acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 15686 and SEQ ID NO: 15687 through SEQ ID NO: 24143 or fragment thereof.

A homologue protein may be derived from, but not limited to, alfalfa, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, pea, peanut, pepper, potato, rye, sorghum, strawberry, sugarcane, sugar-beet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, *Phaseolus* etc. Particularly preferred species for use in the isolation of homologs would include, barley, cotton, oat, oilseed rape, canola, ornamentals, sugarcane, sugarbeet, tomato, potato, wheat and turf grasses. Such a homologue can be obtained by any of a variety of methods. Most preferably, as indicated above, one or more of the disclosed sequences (such as SEQ ID NO: 1287 through SEQ ID NO: 3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof) will be used in defining a pair of primers to isolate the homologue-encoding nucleic acid molecules from any desired species. Such molecules can be expressed to yield protein homologues by recombinant means.

(d) Plant Constructs and Plant Transformants

One or more of the nucleic acid molecules of the invention may be used in plant transformation or transfection. Exogenous genetic material may be transferred into a plant cell and the plant cell regenerated into a whole, fertile or sterile plant. Exogenous genetic material is any genetic material, whether naturally occurring or otherwise, from any source that is capable of being inserted into any organism. In a preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the present invention, preferably a nucleic acid molecule having at least 20 nucleotides of a sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 and complements thereof.

Such genetic material may be transferred into either monocotyledons and dicotyledons including, but not limited to alfalfa, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, pea, peanut, pepper, potato, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, *Phaseolus* etc (Christou, In: *Particle Bombardment for Genetic Engineering of Plants*, Biotechnology Intelligence Unit. Academic Press, San Diego, California (1996)).

Transfer of a nucleic acid that encodes for a protein can result in overexpression of that protein in a transformed cell or transgenic plant. One or more of the proteins or fragments thereof encoded by nucleic acid molecules of the invention may be overexpressed in a transformed cell or transformed plant. Such overexpression may be the result of transient or stable transfer of the exogenous genetic material.

Exogenous genetic material may be transferred into a host cell by the use of a DNA vector or construct designed for such a purpose. Design of such a vector is generally within the skill of the art (*See*, *Plant Molecular Biology: A Laboratory Manual*, Clark (ed.), Springier, New York (1997)).

A construct or vector may include a plant promoter to express the protein or protein fragment of choice. A number of promoters, which are active in plant cells, have been described in the literature. These include the nopaline synthase (NOS) promoter

(Ebert *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 84*:5745-5749 (1987), the octopine synthase (OCS) promoter (which are carried on tumor-inducing plasmids of *Agrobacterium tumefaciens*), the caulimovirus promoters such as the cauliflower mosaic virus (CaMV) 19S promoter (Lawton *et al.*, *Plant Mol. Biol. 9*:315-324 (1987)) and the CaMV 35S promoter (Odell *et al.*, *Nature 313*:810-812 (1985)), the figwort mosaic virus 35S-promoter, the light-inducible promoter from the small subunit of ribulose-1,5-bis-phosphate carboxylase (ssRUBISCO), the Adh promoter (Walker *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 84*:6624-6628 (1987)), the sucrose synthase promoter (Yang *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 87*:4144-4148 (1990)), the R gene complex promoter (Chandler *et al.*, *The Plant Cell 1*:1175-1183 (1989)) and the chlorophyll a/b binding protein gene promoter, etc. These promoters have been used to create DNA constructs that have been expressed in plants; *see, e.g.*, PCT publication WO 84/02913. The CaMV 35S promoters are preferred for use in plants. Promoters known or found to cause transcription of DNA in plant cells can be used in the invention.

For the purpose of expression in source tissues of the plant, such as the leaf, seed, root or stem, it is preferred that the promoters utilized have relatively high expression in these specific tissues. Tissue-specific expression of a protein of the present invention is a particularly preferred embodiment. For this purpose, one may choose from a number of promoters for genes with tissue- or cell-specific or -enhanced expression. Examples of such promoters reported in the literature include the chloroplast glutamine synthetase GS2 promoter from pea (Edwards *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 87*:3459-3463 (1990)), the chloroplast fructose-1,6-biphosphatase (FBPase) promoter from wheat (Lloyd *et al.*, *Mol. Gen. Genet. 225*:209-216 (1991)), the nuclear photosynthetic ST-LS1 promoter from potato (Stockhaus *et al.*, *EMBO J. 8*:2445-2451 (1989)), the serine/threonine kinase (PAL) promoter and the glucoamylase (CHS) promoter from *Arabidopsis thaliana*. Also reported to be active in photosynthetically active tissues are the ribulose-1,5-bisphosphate carboxylase (RbcS) promoter from eastern larch (*Larix laricina*), the promoter for the *cab* gene, cab6, from pine (Yamamoto *et al.*, *Plant Cell Physiol. 35*:773-778 (1994)), the promoter for the Cab-1 gene from wheat (Fejes *et al.*, *Plant Mol. Biol. 15*:921-932 (1990)), the promoter for the CAB-1 gene from spinach (Lubberstedt *et al.*,

Plant Physiol. 104:997-1006 (1994)), the promoter for the cab1R gene from rice (Luan *et al.*, *Plant Cell. 4*:971-981 (1992)), the pyruvate, orthophosphate dikinase (PPDK) promoter from maize (Matsuoka *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 90*: 9586-9590 (1993)), the promoter for the tobacco Lhcb1*2 gene (Cerdan *et al.*, *Plant Mol. Biol. 33*:245-255 (1997)), the *Arabidopsis thaliana* SUC2 sucrose-H+ symporter promoter (Truernit *et al.*, *Planta. 196*:564-570 (1995)) and the promoter for the thylakoid membrane proteins from spinach (psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS). Other promoters for the chlorophyll a/b-binding proteins may also be utilized in the invention, such as the promoters for LhcB gene and PsbP gene from white mustard (*Sinapis alba*; Kretsch *et al.*, *Plant Mol. Biol. 28*:219-229 (1995)).

For the purpose of expression in sink tissues of the plant, such as the tuber of the potato plant, the fruit of tomato, or the seed of maize, wheat, rice and barley, it is preferred that the promoters utilized in the invention have relatively high expression in these specific tissues. A number of promoters for genes with tuber-specific or -enhanced expression are known, including the class I patatin promoter (Bevan *et al.*, *EMBO J. 8*:1899-1906 (1986); Jefferson *et al.*, *Plant Mol. Biol. 14*:995-1006 (1990), the promoter for the potato tuber ADPGPP genes, both the large and small subunits, the sucrose synthase promoter (Salanoubat and Belliard, *Gene 60*:47-56 (1987)), Salanoubat and Belliard, *Gene 84*:181-185 (1989), the promoter for the major tuber proteins including the 22 kd protein complexes and proteinase inhibitors (Hannapel, *Plant Physiol. 101*:703-704 (1993), the promoter for the granule bound starch synthase gene (GBSS) (Visser *et al.*, *Plant Mol. Biol. 17*:691-699 (1991)) and other class I and II patatins promoters (Koster-Topfer *et al.*, *Mol Gen Genet. 219*:390-396 (1989); Mignery *et al.*, *Gene. 62*:27-44 (1988)).

Other promoters can also be used to express a protein or fragment thereof in specific tissues, such as seeds or fruits. The promoter for β-conglycinin (Chen *et al.*, *Dev. Genet. 10*: 112-122 (1989)) or other seed-specific promoters such as the napin and phaseolin promoters, can be used. The zeins are a group of storage proteins found in maize endosperm. Genomic clones for zein genes have been isolated (Pedersen *et al.*, *Cell 29*:1015-1026 (1982)) and the promoters from these clones, including the 15 kD, 16

kD, 19 kD, 22 kD, 27 kD and genes, could also be used. Other promoters known to function, for example, in maize include the promoters for the following genes: *waxy, Brittle, Shrunken 2*, Branching enzymes I and II, starch synthases, debranching enzymes, oleosins, glutelins and sucrose synthases. A particularly preferred promoter for maize endosperm expression is the promoter for the glutelin gene from rice, more particularly the Osgt-1 promoter (Zheng *et al., Mol. Cell Biol. 13*:5829-5842 (1993)). Examples of promoters suitable for expression in wheat include those promoters for the ADPglucose pyrosynthase (ADPGPP) subunits, the granule bound and other starch synthase, the branching and debranching enzymes, the embryogenesis-abundant proteins, the gliadins and the glutenins. Examples of such promoters in rice include those promoters for the ADPGPP subunits, the granule bound and other starch synthase, the branching enzymes, the debranching enzymes, sucrose synthases and the glutelins. A particularly preferred promoter is the promoter for rice glutelin, Osgt-1. Examples of such promoters for barley include those for the ADPGPP subunits, the granule bound and other starch synthase, the branching enzymes, the debranching enzymes, sucrose synthases, the hordeins, the embryo globulins and the aleurone specific proteins.

Root specific promoters may also be used. An example of such a promoter is the promoter for the acid chitinase gene (Samac *et al., Plant Mol. Biol. 25*:587-596 (1994)). Expression in root tissue could also be accomplished by utilizing the root specific subdomains of the CaMV35S promoter that have been identified (Lam *et al., Proc. Natl. Acad. Sci. (U.S.A.) 86*:7890-7894 (1989)). Other root cell specific promoters include those reported by Conkling *et al.* (Conkling *et al., Plant Physiol. 93*:1203-1211 (1990)).

Additional promoters that may be utilized are described, for example, in U.S. Patent Nos. 5,378,619; 5,391,725; 5,428,147; 5,447,858; 5,608,144; 5,608,144; 5,614,399; 5,633,441; 5,633,435; and 4,633,436. In addition, a tissue specific enhancer may be used (Fromm *et al., The Plant Cell 1*:977-984 (1989)).

Constructs or vectors may also include, with the coding region of interest, a nucleic acid sequence that acts, in whole or in part, to terminate transcription of that region. A number of such sequences have been isolated, including the Tr7 3' sequence

and the NOS 3' sequence (Ingelbrecht *et al.*, *The Plant Cell 1*:671-680 (1989); Bevan *et al.*, *Nucleic Acids Res. 11*:369-385 (1983))

A vector or construct may also include regulatory elements. Examples of such include the Adh intron 1 (Callis *et al.*, *Genes and Develop. 1*:1183-1200 (1987)), the sucrose synthase intron (Vasil *et al.*, *Plant Physiol. 91*:1575-1579 (1989)) and the TMV omega element (Gallie *et al.*, *The Plant Cell 1*:301-311 (1989)). These and other regulatory elements may be included when appropriate.

A vector or construct may also include a selectable marker. Selectable markers may also be used to select for plants or plant cells that contain the exogenous genetic material. Examples of such include, but are not limited to: a neomycin phosphotransferase gene (U.S. Patent 5,034,322), which codes for kanamycin resistance and can be selected for using kanamycin, G418, etc.; a bar gene which codes for bialaphos resistance; genes which encode glyphosate resistance (U.S. Patents 4,940,835; 5,188,642; 4,971,908; 5,627,061); a nitrilase gene which confers resistance to bromoxynil (Stalker *et al.*, *J. Biol. Chem. 263*:6310-6314 (1988)); a mutant acetolactate synthase gene (ALS) which confers imidazolinone or sulphonylurea resistance (European Patent Application 154,204 (Sept. 11, 1985)); and a methotrexate resistant DHFR gene (Thillet *et al.*, *J. Biol. Chem. 263*:12500-12508 (1988)).

A vector or construct may also include DNA sequence which encodes a transit peptide. Incorporation of a suitable chloroplast transit peptide may also be employed (European Patent Application Publication Number 0218571). Translational enhancers may also be incorporated as part of the vector DNA. DNA constructs could contain one or more 5' non-translated leader sequences which may serve to enhance expression of the gene products from the resulting mRNA transcripts. Such sequences may be derived from the promoter selected to express the gene or can be specifically modified to increase translation of the mRNA. Such regions may also be obtained from viral RNAs, from suitable eukaryotic genes, or from a synthetic gene sequence. For a review of optimizing expression of transgenes, see Koziel *et al.*, *Plant Mol. Biol. 32*:393-405 (1996) .

A vector or construct may also include a screenable marker. Screenable markers may be used to monitor expression. Exemplary screenable markers include: a β-glucuro-

nidase or uidA gene (GUS) which encodes an enzyme for which various chromogenic substrates are known (Jefferson, *Plant Mol. Biol. Rep. 5*:387-405 (1987); Jefferson *et al.*, *EMBO J. 6*:3901-3907 (1987)); an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (Dellaporta *et al.*, Stadler Symposium *11*:263-282 (1988)); a β-lactamase gene (Sutcliffe *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 75*:3737-3741 (1978)), a gene which encodes an enzyme for which various chromogenic substrates are known (*e.g.*, PADAC, a chromogenic cephalosporin); a luciferase gene (Ow *et al.*, *Science 234*:856-859 (1986)); a xylE gene (Zukowsky *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 80*:1101-1105 (1983)) which encodes a catechol dioxygenase that can convert chromogenic catechols; an α-amylase gene (Ikatu *et al.*, *Bio/Technol. 8*:241-242 (1990)); a tyrosinase gene (Katz *et al.*, *J. Gen. Microbiol. 129*:2703-2714 (1983)) which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to melanin; an α-galactosidase, which will turn a chromogenic α-galactose substrate.

Included within the terms "selectable or screenable marker genes" are also genes which encode a secretable marker whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected catalytically. Secretable proteins fall into a number of classes, including small, diffusible proteins which are detectable, (*e.g.*, by ELISA), small active enzymes which are detectable in extracellular solution (*e.g.*, α-amylase, β-lactamase, phosphinothricin transferase), or proteins which are inserted or trapped in the cell wall (such as proteins which include a leader sequence such as that found in the expression unit of extension or tobacco PR-S). Other possible selectable and/or screenable marker genes will be apparent to those of skill in the art.

There are many methods for introducing transforming nucleic acid molecules into plant cells. Suitable methods are believed to include virtually any method by which nucleic acid molecules may be introduced into a cell, such as by *Agrobacterium* infection or direct delivery of nucleic acid molecules such as, for example, by PEG-mediated transformation, by electroporation or by acceleration of DNA coated particles, etc (Potrykus,

Ann. Rev. Plant Physiol. Plant Mol. Biol. 42:205-225 (1991); Vasil, *Plant Mol. Biol. 25*:925-937 (1994)). For example, electroporation has been used to transform maize protoplasts (Fromm *et al., Nature 312*:791-793 (1986)).

Other vector systems suitable for introducing transforming DNA into a host plant cell include but are not limited to binary artificial chromosome (BIBAC) vectors (Hamilton *et al., Gene 200*:107-116 (1997)); and transfection with RNA viral vectors (Della-Cioppa *et al., Ann. N.Y. Acad. Sci.* (1996), 792 (Engineering Plants for Commercial Products and Applications), 57-61). Additional vector systems also include plant selectable YAC vectors such as those described in Mullen *et al., Molecular Breeding 4*:449-457 (1988)).

Technology for introduction of DNA into cells is well known to those of skill in the art. Four general methods for delivering a gene into cells have been described: (1) chemical methods (Graham and van der Eb, *Virology* 54:536-539 (1973)); (2) physical methods such as microinjection (Capecchi, *Cell* 22:479-488 (1980)), electroporation (Wong and Neumann, *Biochem. Biophys. Res. Commun. 107*:584-587 (1982); Fromm *et al., Proc. Natl. Acad. Sci. (U.S.A.) 82*:5824-5828 (1985); U.S. Patent No. 5,384,253); and the gene gun (Johnston and Tang, *Methods Cell Biol. 43*:353-365 (1994)); (3) viral vectors (Clapp, *Clin. Perinatol. 20*:155-168 (1993); Lu *et al., J. Exp. Med. 178*:2089-2096 (1993); Eglitis and Anderson, *Biotechniques 6*:608-614 (1988)); and (4) receptor-mediated mechanisms (Curiel *et al., Hum. Gen. Ther. 3*:147-154 (1992), Wagner *et al., Proc. Natl. Acad. Sci. (USA) 89*:6099-6103 (1992)).

Acceleration methods that may be used include, for example, microprojectile bombardment and the like. One example of a method for delivering transforming nucleic acid molecules to plant cells is microprojectile bombardment. This method has been reviewed by Yang and Christou (eds.), *Particle Bombardment Technology for Gene Transfer*, Oxford Press, Oxford, England (1994)). Non-biological particles (microprojectiles) may be coated with nucleic acids and delivered into cells by a propelling force. Exemplary particles include those comprised of tungsten, gold, platinum and the like.

A particular advantage of microprojectile bombardment, in addition to it being an effective means of reproducibly transforming monocots, is that neither the isolation of protoplasts (Cristou *et al.*, *Plant Physiol.* *87*:671-674 (1988)) nor the susceptibility of *Agrobacterium* infection are required. An illustrative embodiment of a method for delivering DNA into maize cells by acceleration is a biolistics α-particle delivery system, which can be used to propel particles coated with DNA through a screen, such as a stainless steel or Nytex screen, onto a filter surface covered with corn cells cultured in suspension. Gordon-Kamm *et al.*, describes the basic procedure for coating tungsten particles with DNA (Gordon-Kamm *et al.*, *Plant Cell 2*:603-618 (1990)). The screen disperses the tungsten nucleic acid particles so that they are not delivered to the recipient cells in large aggregates. A particle delivery system suitable for use with the invention is the helium acceleration PDS-1000/He gun is available from Bio-Rad Laboratories (Bio-Rad, Hercules, California)(Sanford *et al.*, *Technique 3*:3-16 (1991)).

For the bombardment, cells in suspension may be concentrated on filters. Filters containing the cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the gun and the cells to be bombarded.

Alternatively, immature embryos or other target cells may be arranged on solid culture medium. The cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the acceleration device and the cells to be bombarded. Through the use of techniques set forth herein one may obtain up to 1000 or more foci of cells transiently expressing a screenable or selectable marker gene. The number of cells in a focus which express the exogenous gene product 48 hours post-bombardment often range from one to ten and average one to three.

In bombardment transformation, one may optimize the pre-bombardment culturing conditions and the bombardment parameters to yield the maximum numbers of stable transformants. Both the physical and biological parameters for bombardment are important in this technology. Physical factors are those that involve manipulating the DNA/ microprojectile precipitate or those that affect the flight and velocity of either the macro-

or microprojectiles. Biological factors include all steps involved in manipulation of cells before and immediately after bombardment, the osmotic adjustment of target cells to help alleviate the trauma associated with bombardment and also the nature of the transforming DNA, such as linearized DNA or intact supercoiled plasmids. It is believed that pre-bombardment manipulations are especially important for successful transformation of immature embryos.

In another alternative embodiment, plastids can be stably transformed. Methods disclosed for plastid transformation in higher plants include the particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination (Svab *et al., Proc. Natl. Acad. Sci. (U.S.A.) 87*:8526-8530 (1990); Svab and Maliga, *Proc. Natl. Acad. Sci. (U.S.A.) 90*:913-917 (1993); Staub and Maliga, *EMBO J. 12*:601-606 (1993); U.S. Patents 5, 451,513 and 5,545,818).

Accordingly, it is contemplated that one may wish to adjust various aspects of the bombardment parameters in small-scale studies to fully optimize the conditions. One may particularly wish to adjust physical parameters such as gap distance, flight distance, tissue distance and helium pressure. One may also minimize the trauma reduction factors by modifying conditions which influence the physiological state of the recipient cells and which may therefore influence transformation and integration efficiencies. For example, the osmotic state, tissue hydration and the subculture stage or cell cycle of the recipient cells may be adjusted for optimum transformation. The execution of other routine adjustments will be known to those of skill in the art in light of the present disclosure.

Agrobacterium-mediated transfer is a widely applicable system for introducing genes into plant cells because the DNA can be introduced into whole plant tissues, thereby bypassing the need for regeneration of an intact plant from a protoplast. The use of *Agrobacterium*-mediated plant integrating vectors to introduce DNA into plant cells is well known in the art. See, for example the methods described by Fraley *et al., Bio/Technology 3*:629-635 (1985) and Rogers *et al., Methods Enzymol. 153*:253-277 (1987). Further, the integration of the Ti-DNA is a relatively precise process resulting in few rearrangements. The region of DNA to be transferred is defined by the border

sequences and intervening DNA is usually inserted into the plant genome as described (Spielmann *et al., Mol. Gen. Genet. 205*:34 (1986)).

Modern *Agrobacterium* transformation vectors are capable of replication in *E. coli* as well as *Agrobacterium*, allowing for convenient manipulations as described (Klee *et al.*, In: *Plant DNA Infectious Agents*, Hohn and Schell (eds.), Springer-Verlag, New York, pp. 179-203 (1985)). Moreover, technological advances in vectors for *Agrobacterium*-mediated gene transfer have improved the arrangement of genes and restriction sites in the vectors to facilitate construction of vectors capable of expressing various polypeptide coding genes. The vectors described have convenient multi-linker regions flanked by a promoter and a polyadenylation site for direct expression of inserted polypeptide coding genes and are suitable for present purposes (Rogers *et al., Methods Enzymol. 153*:253-277 (1987)). In addition, *Agrobacterium* containing both armed and disarmed Ti genes can be used for the transformations. In those plant strains where *Agrobacterium*-mediated transformation is efficient, it is the method of choice because of the facile and defined nature of the gene transfer.

A transgenic plant formed using *Agrobacterium* transformation methods typically contains a single gene on one chromosome. Such transgenic plants can be referred to as being heterozygous for the added gene. More preferred is a transgenic plant that is homozygous for the added structural gene; *i.e.*, a transgenic plant that contains two added genes, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) an independent segregant transgenic plant that contains a single added gene, germinating some of the seed produced and analyzing the resulting plants produced for the gene of interest.

It is also to be understood that two different transgenic plants can also be mated to produce offspring that contain two independently segregating, exogenous genes. Selfing of appropriate progeny can produce plants that are homozygous for both added, exogenous genes that encode a polypeptide of interest. Backcrossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated, as is vegetative propagation.

Transformation of plant protoplasts can be achieved using methods based on calcium phosphate precipitation, polyethylene glycol treatment, electroporation and

combinations of these treatments (*See, for example*, Potrykus *et al.*, *Mol. Gen. Genet. 205*:193-200 (1986); Lorz *et al.*, *Mol. Gen. Genet. 199*:178 (1985); Fromm *et al.*, *Nature 319*:791 (1986); Uchimiya *et al.*, *Mol. Gen. Genet. 204*:204 (1986); Marcotte *et al.*, *Nature 335*:454-457 (1988)).

Application of these systems to different plant strains depends upon the ability to regenerate that particular plant strain from protoplasts. Illustrative methods for the regeneration of cereals from protoplasts are described (Fujimura *et al.*, *Plant Tissue Culture Letters 2*:74 (1985); Toriyama *et al.*, *Theor Appl. Genet. 205*:34 (1986); Yamada *et al.*, *Plant Cell Rep. 4*:85 (1986); Abdullah *et al.*, *Biotechnology 4*:1087 (1986)).

To transform plant strains that cannot be successfully regenerated from protoplasts, other ways to introduce DNA into intact cells or tissues can be utilized. For example, regeneration of cereals from immature embryos or explants can be effected as described (Vasil, *Biotechnology 6*:397 (1988)). In addition, "particle gun" or high-velocity microprojectile technology can be utilized (Vasil *et al.*, *Bio/Technology 10*:667 (1992)).

Using the latter technology, DNA is carried through the cell wall and into the cytoplasm on the surface of small metal particles as described (Klein *et al.*, *Nature 328*:70 (1987); Klein *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 85*:8502-8505 (1988); McCabe *et al.*, *Bio/Technology 6:923* (1988)). The metal particles penetrate through several layers of cells and thus allow the transformation of cells within tissue explants.

The regeneration, development and cultivation of plants from single plant protoplast transformants or from various transformed explants are well known in the art (Weissbach and Weissbach, In: *Methods for Plant Molecular Biology*, Academic Press, San Diego, CA, (1988)). This regeneration and growth process typically includes the steps of selection of transformed cells, culturing those individualized cells through the usual stages of embryonic development through the rooted plantlet stage. Transgenic embryos and seeds are similarly regenerated. The resulting transgenic rooted shoots are thereafter planted in an appropriate plant growth medium such as soil.

The development or regeneration of plants containing the foreign, exogenous gene that encodes a protein of interest is well known in the art. Preferably, the regenerated

plants are self-pollinated to provide homozygous transgenic plants. Otherwise, pollen obtained from the regenerated plants is crossed to seed-grown plants of agronomically important lines. Conversely, pollen from plants of these important lines is used to pollinate regenerated plants. A transgenic plant of the invention containing a desired polypeptide is cultivated using methods well known to one skilled in the art.

There are a variety of methods for the regeneration of plants from plant tissue. The particular method of regeneration will depend on the starting plant tissue and the particular plant species to be regenerated.

Methods for transforming dicots, primarily by use of *Agrobacterium tumefaciens* and obtaining transgenic plants have been published for cotton (U.S. Patent No. 5,004,863; U.S. Patent No. 5,159,135; U.S. Patent No. 5,518,908); soybean (U.S. Patent No. 5,569,834; U.S. Patent No. 5,416,011; McCabe *et. al., Biotechnology 6*:923 (1988); Christou *et al., Plant Physiol. 87*:671-674 (1988)); *Brassica* (U.S. Patent No. 5,463,174); peanut (Cheng *et al., Plant Cell Rep. 15*:653-657 (1996), McKently *et al., Plant Cell Rep. 14*:699-703 (1995)); papaya; and pea (Grant *et al., Plant Cell Rep. 15*:254-258 (1995)).

Transformation of monocotyledons using electroporation, particle bombardment and *Agrobacterium* have also been reported. Transformation and plant regeneration have been achieved in asparagus (Bytebier *et al., Proc. Natl. Acad. Sci. (USA) 84*:5354 (1987)); barley (Wan and Lemaux, *Plant Physiol 104*:37 (1994)); maize (Rhodes *et al., Science 240*:204 (1988); Gordon-Kamm *et al., Plant Cell* 2:603-618 (1990); Fromm *et al., Bio/Technology 8*:833 (1990); Koziel *et al., Bio/Technology 11*:194 (1993); Armstrong *et al., Crop Science 35*:550-557 (1995)); oat (Somers *et al., Bio/Technology 10*:1589 (1992)); orchard grass (Horn *et al., Plant Cell Rep. 7*:469 (1988)); rice (Toriyama *et al., Theor Appl. Genet. 205*:34 (1986); Part *et al., Plant Mol. Biol. 32*:1135-1148 (1996); Abedinia *et al., Aust. J. Plant Physiol. 24*:133-141 (1997); Zhang and Wu, *Theor. Appl. Genet. 76*:835 (1988); Zhang *et al., Plant Cell Rep. 7*:379 (1988); Battraw and Hall, *Plant Sci. 86*:191-202 (1992); Christou *et al., Bio/Technology 9*:957 (1991); rye (De la Pena *et al., Nature 325*:274 (1987)); sugarcane (Bower and Birch, *Plant J. 2*:409 (1992); tall fescue (Wang *et al., Bio/Technology 10*:691 (1992) and wheat (Vasil *et al., Bio/Technology 10*:667 (1992); U.S. Patent No. 5,631,152)).

Assays for gene expression based on the transient expression of cloned nucleic acid constructs have been developed by introducing the nucleic acid molecules into plant cells by polyethylene glycol treatment, electroporation, or particle bombardment (Marcotte *et al., Nature 335*:454-457 (1988); Marcotte *et al., Plant Cell 1*:523-532 (1989); McCarty *et al., Cell 66*:895-905 (1991); Hattori *et al., Genes Dev. 6*:609-618 (1992); Goff *et al., EMBO J. 9*:2517-2522 (1990)). Transient expression systems may be used to functionally dissect gene constructs (*see generally*, Mailga *et al., Methods in Plant Molecular Biology*, Cold Spring Harbor Press (1995)).

Any of the nucleic acid molecules of the invention may be introduced into a plant cell in a permanent or transient manner in combination with other genetic elements such as vectors, promoters, enhancers, *etc*. Further, any of the nucleic acid molecules of the invention may be introduced into a plant cell in a manner that allows for overexpression of the protein or fragment thereof encoded by the nucleic acid molecule.

Cosuppression is the reduction in expression levels, usually at the level of RNA, of a particular endogenous gene or gene family by the expression of a homologous sense construct that is capable of transcribing mRNA of the same strandedness as the transcript of the endogenous gene (Napoli *et al., Plant Cell 2*:279-289 (1990); van der Krol *et al., Plant Cell 2*:291-299 (1990)). Cosuppression may result from stable transformation with a single copy nucleic acid molecule that is homologous to a nucleic acid sequence found within the cell (Prolls and Meyer, *Plant J. 2*:465-475 (1992)) or with multiple copies of a nucleic acid molecule that is homologous to a nucleic acid sequence found within the cell (Mittlesten *et al., Mol. Gen. Genet. 244*:325-330 (1994)). Genes, even though different, linked to homologous promoters may result in the cosuppression of the linked genes (Vaucheret, *C.R. Acad. Sci. III 316*:1471-1483 (1993); Flavell, *Proc. Natl. Acad. Sci. (U.S.A.) 91*:3490-3496 (1994)); van Blokland *et al., Plant J. 6*:861-877 (1994); Jorgensen, *Trends Biotechnol. 8*:340-344 (1990); Meins and Kunz, In: *Gene Inactivation and Homologous Recombination in Plants*, Paszkowski (ed.), pp. 335-348, Kluwer Academic, Netherlands (1994)).

It is understood that one or more of the nucleic acids of the invention may be introduced into a plant cell and transcribed using an appropriate promoter with such transcription resulting in the cosuppression of an endogenous protein.

Antisense approaches are a way of preventing or reducing gene function by targeting the genetic material (U.S. Patents 4,801,540 and 5,107,065 Mol *et al.*, *FEBS Lett. 268*:427-430 (1990)). The objective of the antisense approach is to use a sequence complementary to the target gene to block its expression and create a mutant cell line or organism in which the level of a single chosen protein is selectively reduced or abolished. Antisense techniques have several advantages over other 'reverse genetic' approaches. The site of inactivation and its developmental effect can be manipulated by the choice of promoter for antisense genes or by the timing of external application or microinjection. Antisense can manipulate its specificity by selecting either unique regions of the target gene or regions where it shares homology to other related genes (Hiatt *et al.*, In: *Genetic Engineering*, Setlow (ed.), Vol. 11, New York: Plenum 49-63 (1989)).

The principle of regulation by antisense RNA is that RNA that is complementary to the target mRNA is introduced into cells, resulting in specific RNA:RNA duplexes being formed by base pairing between the antisense substrate and the target mRNA (Green *et al.*, *Annu. Rev. Biochem. 55*:569-597 (1986)). Under one embodiment, the process involves the introduction and expression of an antisense gene sequence. Such a sequence is one in which part or all of the normal gene sequences are placed under a promoter in inverted orientation so that the 'wrong' or complementary strand is transcribed into a noncoding antisense RNA that hybridizes with the target mRNA and interferes with its expression (Takayama and Inouye, *Crit. Rev. Biochem. Mol. Biol. 25*:155-184 (1990)). An antisense vector is constructed by standard procedures and introduced into cells by transformation, transfection, electroporation, microinjection, infection, etc. The type of transformation and choice of vector will determine whether expression is transient or stable. The promoter used for the antisense gene may influence the level, timing, tissue, specificity, or inducibility of the antisense inhibition.

It is understood that the activity of a protein in a plant cell may be reduced or depressed by growing a transformed plant cell containing a nucleic acid molecule whose non-transcribed strand encodes a protein or fragment thereof.

Post transcriptional gene silencing (PTGS) can result in virus immunity or gene silencing in plants. PTGS is induced by dsRNA and is mediated by an RNA-dependent RNA polymerase, present in the cytoplasm, that requires a dsRNA template. The dsRNA is formed by hybridization of complementary transgene mRNAs or complementary regions of the same transcript. Duplex formation can be accomplished by using transcripts from one sense gene and one antisense gene co-located in the plant genome, a single transcript that has self-complementarity, or sense and antisense transcripts from genes brought together by crossing. The dsRNA-dependent RNA polymerase makes a complementary strand from the transgene mRNA and RNAse molecules attach to this complementary strand (cRNA). These cRNA-RNAse molecules hybridize to the endogene mRNA and cleave the single-stranded RNA adjacent to the hybrid. The cleaved single-stranded RNAs are further degraded by other host RNAses because one will lack a capped 5' end and the other will lack a poly(A) tail (Waterhouse *et al.*, *PNAS 95*: 13959-13964 (1998)).

It is understood that one or more of the nucleic acids of the invention may be introduced into a plant cell and transcribed using an appropriate promoter with such transcription resulting in the postranscriptional gene silencing of an endogenous transcript.

Homologous recombination may be used to prevent gene function (Capecchi, M.R. *Science*, *244*:1288-1292(1989)). In one example, a gene to be knocked out may be interrupted with a selectable marker gene that lacks its own promoter. After transformation, selection for the marker is applied. Few heterologous insertions result in the incorporation of the marker gene into a genomic sequence encoding an mRNA, so the marker is rarely expressed. Homologous recombination results in the incorporation of the marker into the transcription unit of the target gene, allowing marker expression and the survival of the cell during the selection.

Gene targeting can also be performed without the use of selection (Capecchi, M.R. *Science*, *244*:1288-1292(1989), Bollag *et. al. Ann. Rev. Gen. 23*:199-224 (1989)). For example, a gene can be knocked out with a copy of the gene containing an insertion disrupting the reading frame and the transformed cells can then be analyzed by the PCR reaction. The PCR uses two primers, one that anneals to the inserted sequence and one that anneals to the native DNA beyond the end of the transformed fragment. In the event of homologous recombination, only, will the PCR yield a fragment of the expected size.

It is understood that one or more of the nucleic acids of the invention may be included in a "Knockout construct" meaning that a DNA sequence has been altered via any known means, for example, deletion, insertion, point mutation or rearrangement, so as to eliminate the function of the naturally occurring nucleic acid sequence, but not so as to alter the ability of the DNA sequence to recombine with the naturally-occurring sequence United States Patent 5,952,548.

Insertion mutations created by insertion elements may also prevent gene function (United States Patent 6,013,486). For example, in many dicot plants, transformation with the T-DNA of *Agrobacterium* may be readily achieved and large numbers of transformants can be rapidly obtained. Also, some species have lines with active transposable elements which can efficiently be used for the generation of large numbers of insertion mutations, while some other species lack such options.

Transposable-elements are a versatile class of insertional mutagen in that a variety of transposable elements have been identified, with representative elements having been found in all eukaryotic genomes examined. As used herein, the term "transposable element" will mean any mobile genetic element which is capable of replicative or non-replicative transposition within a genome, causing insertional mutagenesis at the site of insertion. One example of a transposable element of maize contemplated to have particular utility in the generation of insertion mutations is the Mutator element (Bennetzen, J. *Mol. Appl. Genet.*, *2*:519- 524 (1984); Talbert *et al. J. Mol. Evol.*, *29*:28-39 (1989)), see Genbank Accession Numbers: x14224, x14225, g22495, g22466, g22373, m76978 and x97569). Other examples of transposable elements which are deemed particularly useful insertional mutagens are the Ac element (Geiser *et al. The EMBO*

Journal, 1:1455- 1460 (1982), 1982; U.S. Pat. No. 4,732,856, and the tobacco element slide-124 (Genbank Accession Number x97569)).

One preferred method which may be used for the selection and identification of insertional mutants obtained by transformation or transposable elements is described in United States Patent 6,013,486. Briefly, an insertion event in a genome is identified by first preparing a "DNA Composition Enhanced for a Plurality of Insertion Junctions". This phrase is defined as a DNA composition in which a non-locus specific selection of insertion junctions (the segment of DNA encompassing the end of an insertional mutagen and particularly, the flanking genomic DNA into which the insertional mutagen has inserted) has been enhanced relative to the starting DNA from which the DNA composition is derived. Such non-locus specific selections are prepared without the need for use of probes or primers which are specific to the locus or loci for which an insertion mutation is desired. The selection procedure will typically, instead, use probes or primers which are specific to the insertional mutagen. Examples of such procedures include inverse PCR (U.S. Pat. No. 4,994,370), primer adapted PCR (Mueller *et al., Science, 246*:78-786 (1989)), and vectorette PCR (European Patent No. 0 439 330), AIMS (Souer *et al., The Plant Journal, 7*(4):677-685, 1995)), or any other amplification or isolation procedure which is capable of being used to enhance a DNA composition for a diverse class of insertion junctions. Secondly, sequences from this DNA composition are arranged on a "detectable array". A detectable array is an arrangement of nucleic acid sequences from which specific sequences or subsets of sequences can be identified. The array can comprise DNA sequences bound to a solid support and can also include DNA compositions arranged in solution in suitable containers. The sequences will be ones which may be used to identify one or more specific insertion junctions. These sequences can, therefore, represent DNA of insertion junctions or, alternatively, sequences representing a particular locus for which an insertion mutation is desired. The insertion event can be identified by hybridizing gene-specific probes or using the PCR with gene-specific primers.

It is understood that one or more of the nucleic acid sequences of this invention may be used as probes or primers to detect insertion events according to the method described in United States Patent 6,013,486

Other methods to detect insertion events may also use the PCR. Further PCR-related examples of insertion detection can be found in, but are not limited to: Ballinger *et al., Proc. Natl. Acad. Sci. USA, 86*:9402-9406 (1989), Rushforth, A. M., *et al., Mol. Cell. Biol., 13*:029-910 (1993), Zwaal, R.R., *et al., Proc. Natl. Acad. Sci. USA, 90*:7431-7435 (1993), Koes, R. *et al, Proc. Natl. Acad. Sci. USA 92* 8149-8153 (1995), Krysan *et al., Proc. Natl. Acad. Sci. USA 93*, 8145-8150 (1996) and McKinney *et al. Plant J. 8*,613-622. (1995).

It is understood that one or more of the nucleic acid sequences of this invention may be used as primers to detect insertion events.

Antibodies have been expressed in plants (Hiatt *et al., Nature 342:*76-78 (1989); Conrad and Fielder, *Plant Mol. Biol. 26:*1023-1030 (1994)). Cytoplasmic expression of a scFv (single-chain Fv antibodies) has been reported to delay infection by artichoke mottled crinkle virus. Transgenic plants that express antibodies directed against endogenous proteins may exhibit a physiological effect (Philips *et al., EMBO J. 16:*4489-4496 (1997); Marion-Poll, *Trends in Plant Science 2:*447-448 (1997)). For example, expressed anti-abscissic antibodies have been reported to result in a general perturbation of seed development (Philips *et al., EMBO J. 16:* 4489-4496 (1997)).

Antibodies that are catalytic may also be expressed in plants (abzymes). The principle behind abzymes is that since antibodies may be raised against many molecules, this recognition ability can be directed toward generating antibodies that bind transition states to force a chemical reaction forward (Persidas, *Nature Biotechnology 15:*1313-1315 (1997) Baca *et al., Ann. Rev. Biophys. Biomol. Struct. 26:*461-493 (1997)). The catalytic abilities of abzymes may be enhanced by site directed mutagenesis. Examples of abzymes are, for example, set forth in U.S. Patent No: 5,658,753; U.S. Patent No. 5,632,990; U.S. Patent No. 5,631,137; U.S. Patent 5,602,015; U.S. Patent No. 5,559,538; U.S. Patent No. 5,576,174; U.S. Patent No. 5,500,358; U.S. Patent 5,318,897; U.S. Patent No. 5,298,409; U.S. Patent No. 5,258,289 and U.S. Patent No. 5,194,585.

It is understood that any of the antibodies of the invention may be expressed in plants and that such expression can result in a physiological effect. It is also understood that any of the expressed antibodies may be catalytic.

The present invention also provides for parts of the plants of the present invention. Plant parts, without limitation, include seed, endosperm, ovule and pollen. In a particularly preferred embodiment of the present invention, the plant part is a seed.

Exemplary Uses

Nucleic acid molecules and fragments thereof of the invention may be employed to obtain other nucleic acid molecules from the same species (nucleic acid molecules from maize may be utilized to obtain other nucleic acid molecules from maize). Such nucleic acid molecules include the nucleic acid molecules that encode the complete coding sequence of a protein and promoters and flanking sequences of such molecules. In addition, such nucleic acid molecules include nucleic acid molecules that encode for other isozymes or gene family members. Such molecules can be readily obtained by using the above-described nucleic acid molecules or fragments thereof to screen cDNA or genomic libraries. Methods for forming such libraries are well known in the art.

Nucleic acid molecules and fragments thereof of the invention may also be employed to obtain nucleic acid homologues. Such homologues include the nucleic acid molecule of other plants or other organisms (*e.g.*, alfalfa, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, pea, peanut, pepper, potato, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, *Phaseolus*, etc.) including the nucleic acid molecules that encode, in whole or in part, protein homologues of other plant species or other organisms, sequences of genetic elements, such as promoters and transcriptional regulatory elements. Such molecules can be readily obtained by using the above-described nucleic acid molecules or fragments thereof to screen cDNA or genomic libraries obtained from such plant species. Methods for forming such libraries are well known in the art. Such homologue molecules may differ in their nucleotide sequences from those found in one or more of SEQ ID NO:

1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 and complements thereof.

Any of a variety of methods may be used to obtain one or more of the above-described nucleic acid molecules (Zamechik *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *83*:4143-4146 (1986); Goodchild *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *85*:5507-5511 (1988); Wickstrom *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *85*:1028-1032 (1988); Holt *et al.*, *Molec. Cell. Biol.* *8*:963-973 (1988); Gerwirtz *et al.*, *Science* *242*:1303-1306 (1988); Anfossi *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *86*:3379-3383 (1989); Becker *et al.*, *EMBO J.* *8*:3685-3691 (1989)). Automated nucleic acid synthesizers may be employed for this purpose. In lieu of such synthesis, the disclosed nucleic acid molecules may be used to define a pair of primers that can be used with the polymerase chain reaction (Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol.* *51*:263-273 (1986)); Erlich *et al.*, European Patent 50,424; European Patent 84,796; European Patent 258,017; European Patent 237,362; Mullis, European Patent 201,184; Mullis *et al.*, U.S. Patent 4,683,202; Erlich, U.S. Patent 4,582,788; and Saiki *et al.*, U.S. Patent 4,683,194) to amplify and obtain any desired nucleic acid molecule or fragment.

Promoter sequences and other genetic elements, including but not limited to transcriptional regulatory flanking sequences, associated with one or more of the disclosed nucleic acid sequences can also be obtained using the disclosed nucleic acid sequence provided herein. In one embodiment, such sequences are obtained by incubating nucleic acid molecules of the present invention with members of genomic libraries and recovering clones that hybridize to such nucleic acid molecules thereof. In a second embodiment, methods of "chromosome walking," or inverse PCR may be used to obtain such sequences (Frohman *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *85*:8998-9002 (1988); Ohara *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *86*:5673-5677 (1989); Pang *et al.*, *Biotechniques* *22*:1046-1048 (1977); Huang *et al.*, *Methods Mol. Biol.* *69*:89-96 (1997); Huang *et al.*, *Method Mol. Biol.* *67*:287-294 (1997); Benkel *et al.*, *Genet. Anal.* *13*:123-127 (1996); Hartl *et al.*, *Methods Mol. Biol.* *58*:293-301 (1996)). The term "chromosome walking" means a process of extending a genetic map by successive hybridization steps.

The nucleic acid molecules of the invention may be used to isolate promoters of cell enhanced, cell specific, tissue enhanced, tissue specific, developmentally or environmentally regulated expression profiles. Isolation and functional analysis of the 5' flanking promoter sequences of these genes from genomic libraries, for example, using genomic screening methods and PCR techniques would result in the isolation of useful promoters and transcriptional regulatory elements. These methods are known to those of skill in the art and have been described (See, for example, Birren *et al.*, *Genome Analysis: Analyzing DNA*, 1, (1997), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.). Promoters obtained utilizing the nucleic acid molecules of the invention could also be modified to affect their control characteristics. Examples of such modifications would include but are not limited to enhancer sequences. Such genetic elements could be used to enhance gene expression of new and existing traits for crop improvement.

Another subset of the nucleic acid molecules of the invention includes nucleic acid molecules that are markers. The markers can be used in a number of conventional ways in the field of molecular genetics. Such markers include nucleic acid molecules SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof or fragments of either that can act as markers and other nucleic acid molecules of the present invention that can act as markers.

Genetic markers of the invention include "dominant" or "codominant" markers. "Codominant markers" reveal the presence of two or more alleles (two per diploid individual) at a locus. "Dominant markers" reveal the presence of only a single allele per locus. The presence of the dominant marker phenotype (*e.g.*, a band of DNA) is an indication that one allele is in either the homozygous or heterozygous condition. The absence of the dominant marker phenotype (*e.g.*, absence of a DNA band) is merely evidence that "some other" undefined allele is present. In the case of populations where individuals are predominantly homozygous and loci are predominately dimorphic, dominant and codominant markers can be equally valuable. As populations become more heterozygous and multi-allelic, codominant markers often become more informative of

the genotype than dominant markers. Marker molecules can be, for example, capable of detecting polymorphisms such as single nucleotide polymorphisms (SNPs).

SNPs can be characterized using any of a variety of methods (Botstein *et al.*, *Am. J. Hum. Genet. 32*:314-331 (1980); Konieczny and Ausubel, *Plant J. 4*:403-410 (1993); Myers *et al.*, *Nature 313*:495-498 (1985); Newton *et al.*, *Nucl. Acids Res. 17*:2503-2516 (1989); Wu *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 86*:2757-2760 (1989); Barany, *Proc. Natl. Acad. Sci. (U.S.A.) 88*:189-193 (1991); Labrune *et al.*, *Am. J. Hum. Genet. 48*: 1115-1120 (1991); Kuppuswami *et al.*, *Proc. Natl. Acad. Sci. USA 88*:1143-1147 (1991); Sarkar *et al.*, *Genomics 13*:441-443 (1992); Nikiforov *et al.*, *Nucl. Acids Res. 22*:4167-4175 (1994); Livak *et al.*, *PCR Methods Appl. 4*:357-362 (1995); Livak *et al.*, *Nature Genet. 9*:341-342 (1995); Chen and Kwok, *Nucl. Acids Res. 25*:347-353 (1997); Tyagi *et al.*, *Nature Biotech. 16*: 49-53 (1998); Haff and Smirnov, *Genome Res. 7*: 378-388 (1997); Neff *et al.*, *Plant J. 14*:387-392 (1998)).

Additional markers, such as AFLP markers, RFLP markers and RAPD markers, can be utilized (Walton, *Seed World* 22-29 (July, 1993); Burow and Blake, *Molecular Dissection of Complex Traits*, 13-29, Paterson (ed.), CRC Press, New York (1988)). Another marker type, RAPDs, are developed from DNA amplification with random primers and result from single base changes and insertions/deletions in plant genomes. They are dominant markers with a medium level of polymorphisms and are highly abundant. AFLP markers require using the PCR on a subset of restriction fragments from extended adapter primers. These markers are both dominant and codominant are highly abundant in genomes and exhibit a medium level of polymorphism.

The genomes of animals and plants naturally undergo spontaneous mutation in the course of their continuing evolution (Gusella, *Ann. Rev. Biochem. 55*:831-854 (1986)). A "polymorphism" is a variation or difference in the sequence of the gene or its flanking regions that arises in some of the members of a species. The variant sequence and the "original" sequence co-exist in the species' population. In some instances, such co-existence is in stable or quasi-stable equilibrium.

A polymorphism is thus said to be "allelic," in that, due to the existence of the polymorphism, some members of a species may have the original sequence (*i.e.*, the

original "allele") whereas other members may have the variant sequence (*i.e.*, the variant "allele"). In the simplest case, only one variant sequence may exist and the polymorphism is thus said to be di-allelic. In other cases, the species' population may contain multiple alleles and the polymorphism is termed tri-allelic, etc. A single gene may have multiple different unrelated polymorphisms. For example, it may have a di-allelic polymorphism at one site and a multi-allelic polymorphism at another site.

The variation that defines the polymorphism may range from a single nucleotide variation to the insertion or deletion of extended regions within a gene. In some cases, the DNA sequence variations are in regions of the genome that are characterized by short tandem repeats (STRs) that include tandem di- or tri-nucleotide repeated motifs of nucleotides. Polymorphisms characterized by such tandem repeats are referred to as "variable number tandem repeat" ("VNTR") polymorphisms. VNTRs have been used in identity analysis (Weber, U.S. Patent 5,075,217; Armour *et al., FEBS Lett. 307*:113-115 (1992); Jones *et al., Eur. J. Haematol. 39*:144-147 (1987); Horn *et al.*, PCT Patent Application WO91/14003; Jeffreys, European Patent Application 370,719; Jeffreys, U.S. Patent 5,175,082; Jeffreys *et al., Amer. J. Hum. Genet. 39*:11-24 (1986); Jeffreys *et al., Nature 316*:76-79 (1985); Gray *et al., Proc. R. Acad. Soc. Lond. 243*:241-253 (1991); Moore *et al., Genomics 10*:654-660 (1991); Jeffreys *et al., Anim. Genet. 18*:1-15 (1987); Hillel *et al., Anim. Genet. 20*:145-155 (1989); Hillel *et al., Genet. 124*:783-789 (1990)).

The detection of polymorphic sites in a sample of DNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis or other means.

In an alternative embodiment, such polymorphisms can be detected through the use of a marker nucleic acid molecule that is physically linked to such polymorphism(s). For this purpose, marker nucleic acid molecules comprising a nucleotide sequence of a polynucleotide located within 1 mb of the polymorphism(s) and more preferably within 100kb of the polymorphism(s) and most preferably within 10kb of the polymorphism(s) can be employed.

The identification of a polymorphism can be determined in a variety of ways. By correlating the presence or absence of it in a plant with the presence or absence of a phenotype, it is possible to predict the phenotype of that plant. If a polymorphism creates or destroys a restriction endonuclease cleavage site, or if it results in the loss or insertion of DNA (*e.g.*, a VNTR polymorphism), it will alter the size or profile of the DNA fragments that are generated by digestion with that restriction endonuclease. As such, individuals that possess a variant sequence can be distinguished from those having the original sequence by restriction fragment analysis. Polymorphisms that can be identified in this manner are termed "restriction fragment length polymorphisms" ("RFLPs") (Glassberg, UK Patent Application 2135774; Skolnick *et al.*, *Cytogen. Cell Genet. 32*:58-67 (1982); Botstein *et al.*, *Ann. J. Hum. Genet. 32*:314-331 (1980); Fischer *et al.*, (PCT Application WO90/13668; Uhlen, PCT Application WO90/11369).

Polymorphisms can also be identified by Single Strand Conformation Polymorphism (SSCP) analysis (Elles, *Methods in Molecular Medicine: Molecular Diagnosis of Genetic Diseases*, Humana Press (1996); Orita *et al.*, *Genomics 5*:874-879 (1989)). A number of protocols have been described for SSCP including, but not limited to, Lee *et al.*, *Anal. Biochem. 205*:289-293 (1992); Suzuki *et al.*, *Anal. Biochem. 192*:82-84 (1991); Lo *et al.*, *Nucleic Acids Research 20*:1005-1009 (1992); Sarkar *et al.*, *Genomics 13*:441-443 (1992). It is understood that one or more of the nucleic acids of the invention, may be utilized as markers or probes to detect polymorphisms by SSCP analysis or to identify genetically linked molecular markers.

Polymorphisms may also be found using a DNA fingerprinting technique called amplified fragment length polymorphism (AFLP), which is based on the selective PCR amplification of restriction fragments from a total digest of genomic DNA to profile that DNA (Vos *et al.*, *Nucleic Acids Res. 23*:4407-4414 (1995)). This method allows for the specific co-amplification of high numbers of restriction fragments, which can be visualized by PCR without knowledge of the nucleic acid sequence. It is understood that one or more of the nucleic acids of the invention, may be utilized as markers or probes to detect polymorphisms by AFLP analysis or for fingerprinting RNA.

Polymorphisms may also be found using random amplified polymorphic DNA (RAPD) (Williams *et al., Nucl. Acids Res. 18*:6531-6535 (1990)) and cleaveable amplified polymorphic sequences (CAPS) (Lyamichev *et al., Science 260*:778-783 (1993)). It is understood that one or more of the nucleic acid molecules of the invention, may be utilized as markers or probes to detect polymorphisms by RAPD or CAPS analysis or identifying genetically linked molecular markers.

Through genetic mapping, a fine scale linkage map can be developed using DNA markers and, then, a genomic DNA library of large-sized fragments can be screened with molecular markers linked to the desired trait. Molecular markers are advantageous for agronomic traits that are otherwise difficult to tag, such as resistance to pathogens, insects and nematodes, tolerance to abiotic stress, quality parameters and quantitative traits such as high yield potential. Here, an altered phytosterol level are preferred traits.

Essential requirements for marker-assisted selection in a plant breeding program are: (1) the marker(s) should co-segregate or be closely linked with the desired trait; (2) an efficient means of screening large populations for the molecular marker(s) should be available; and (3) the screening technique should have high reproducibility across laboratories and preferably be economical to use and be user-friendly.

The genetic linkage of marker molecules can be established by a gene mapping model such as, without limitation, the flanking marker model reported by Lander and Botstein, *Genetics 121*:185-199 (1989) and the interval mapping, based on maximum likelihood methods described by Lander and Botstein, *Genetics 121*:185-199 (1989) and implemented in the software package MAPMAKER/QTL (Lincoln and Lander, *Mapping Genes Controlling Quantitative Traits Using MAPMAKER/QTL*, Whitehead Institute for Biomedical Research, Massachusetts, (1990). Additional software includes Qgene, Version 2.23 (1996), Department of Plant Breeding and Biometry, 266 Emerson Hall, Cornell University, Ithaca, NY). Use of Qgene software is a particularly preferred approach.

A maximum likelihood estimate (MLE) for the presence of a marker is calculated, together with an MLE assuming no QTL effect, to avoid false positives. A $\log_{10}$ of an

odds ratio (LOD) is then calculated as: LOD = $\log_{10}$(MLE for the presence of a QTL/MLE given no linked QTL).

The LOD score essentially indicates how much more likely the data are to have arisen assuming the presence of a QTL than in its absence. The LOD threshold value for avoiding a false positive with a given confidence, say 95%, depends on the number of markers and the length of the genome. Graphs indicating LOD thresholds are set forth in Lander and Botstein, *Genetics 121*:185-199 (1989) and further described by Arús and Moreno-González . *Plant Breeding*, Hayward *et al.*, (eds.) Chapman & Hall, London, pp. 314-331 (1993).

Additional models can be used. Many modifications and alternative approaches to interval mapping have been reported, including the use non-parametric methods (Kruglyak and Lander, *Genetics 139*:1421-1428 (1995)). Multiple regression methods or models can be also be used, in which the trait is regressed on a large number of markers (Jansen, *Biometrics in Plant Breeding*, van Oijen and Jansen (eds.), Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp. 116-124 (1994); Weber and Wricke, *Advances in Plant Breeding*, Blackwell, Berlin, 16 (1994)). Procedures combining interval mapping with regression analysis, whereby the phenotype is regressed onto a single putative QTL at a given marker interval and at the same time onto a number of markers that serve as 'cofactors,' have been reported by Jansen and Stam, *Genetics 136*:1447-1455 (1994), and Zeng, *Genetics 136*:1457-1468 (1994) . Generally, the use of cofactors reduces the bias and sampling error of the estimated QTL positions (Utz and Melchinger, *Biometrics in Plant Breeding*, van Oijen and Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp.195-204 (1994), thereby improving the precision and efficiency of QTL mapping (Zeng, *Genetics 136*:1457-1468 (1994)). These models can be extended to multi-environment experiments to analyze genotype-environment interactions (Jansen *et al.*, *Theo. Appl. Genet. 91*:33-37 (1995)).

It is understood that one or more of the nucleic acid molecules of the invention may be used as molecular markers. It is also understood that one or more of the protein molecules of the invention may be used as molecular markers.

In accordance with this aspect of the invention, a sample nucleic acid is obtained from plant cells or tissues. Any source of nucleic acid may be used. Preferably, the nucleic acid is genomic DNA. The nucleic acid is subjected to restriction endonuclease digestion. For example, one or more nucleic acid molecule or fragment thereof of the invention can be used as a probe in accordance with the above-described polymorphic methods. The polymorphism obtained in this approach can then be cloned to identify the mutation at the coding region, which alters structure, or regulatory region of the gene, which affects its expression level.

In an aspect of the present invention, one or more of the nucleic molecules of the present invention are used to determine the level (*i.e.*, the concentration of mRNA in a sample, *etc.*) in a plant (preferably maize, soybean, rice or *Arabidopsis*) or pattern (*i.e.*, the kinetics of expression, rate of decomposition, stability profile, *etc.*) of the expression of a protein encoded in part or whole by one or more of the nucleic acid molecule of the present invention (collectively, the "Expression Response" of a cell or tissue).

As used herein, the Expression Response manifested by a cell or tissue is said to be "altered" if it differs from the Expression Response of cells or tissues of plants not exhibiting the phenotype. To determine whether a Expression Response is altered, the Expression Response manifested by the cell or tissue of the plant exhibiting the phenotype is compared with that of a similar cell or tissue sample of a plant not exhibiting the phenotype. As will be appreciated, it is not necessary to re-determine the Expression Response of the cell or tissue sample of plants not exhibiting the phenotype each time such a comparison is made; rather, the Expression Response of a particular plant may be compared with previously obtained values of normal plants. As used herein, the phenotype of the organism is any of one or more characteristics of an organism (*e.g.* disease resistance, pest tolerance, environmental tolerance such as tolerance to abiotic stress, male sterility, quality improvement or yield *etc.*). A change in genotype or phenotype may be transient or permanent. Also as used herein, a tissue sample is any sample that comprises more than one cell. In a preferred aspect, a tissue sample comprises cells that share a common characteristic (*e.g.* derived from root, seed, flower, leaf, stem or pollen etc.).

In one aspect of the present invention, an evaluation can be conducted to determine whether a particular mRNA molecule is present. One or more of the nucleic acid molecules of the present invention are utilized to detect the presence or quantity of the mRNA species. Such molecules are then incubated with cell or tissue extracts of a plant under conditions sufficient to permit nucleic acid hybridization. The detection of double-stranded probe-mRNA hybrid molecules is indicative of the presence of the mRNA; the amount of such hybrid formed is proportional to the amount of mRNA. Thus, such probes may be used to ascertain the level and extent of the mRNA production in a plant's cells or tissues. Such nucleic acid hybridization may be conducted under quantitative conditions (thereby providing a numerical value of the amount of the mRNA present). Alternatively, the assay may be conducted as a qualitative assay that indicates either that the mRNA is present, or that its level exceeds a user set, predefined value.

A number of methods can be used to compare the expression response between two or more samples of cells or tissue. These methods include hybridization assays, such as Northerns, RNAse protection assays, and *in situ* hybridization. Alternatively, the methods include PCR-type assays. In a preferred method, the expression response is compared by hybridizing nucleic acids from the two or more samples to an array of nucleic acids. The array contains a plurality of suspected sequences known or suspected of being present in the cells or tissue of the samples.

An advantage of *in situ* hybridization over more conventional techniques for the detection of nucleic acids is that it allows an investigator to determine the precise spatial population (Angerer *et al., Dev. Biol. 101*:477-484 (1984); Angerer *et al., Dev. Biol. 112*:157-166 (1985); Dixon *et al., EMBO J. 10*:1317-1324 (1991)). *In situ* hybridization may be used to measure the steady-state level of RNA accumulation (Hardin *et al., J. Mol. Biol. 202*:417-431 (1989)). A number of protocols have been devised for *in situ* hybridization, each with tissue preparation, hybridization and washing conditions (Meyerowitz, *Plant Mol. Biol. Rep. 5*:242-250 (1987); Cox and Goldberg, In: *Plant Molecular Biology: A Practical Approach*, Shaw (ed.), pp. 1-35, IRL Press, Oxford (1988); Raikhel *et al., In situ RNA hybridization in plant tissues*, In: *Plant Molecular Biology Manual*, vol. B9:1-32, Kluwer Academic Publisher, Dordrecht, Belgium (1989)).

In situ hybridization also allows for the localization of proteins within a tissue or cell (Wilkinson, *In Situ Hybridization*, Oxford University Press, Oxford (1992); Langdale, *In Situ Hybridization* In: *The Maize Handbook*, Freeling and Walbot (eds.), pp. 165-179, Springer-Verlag, New York (1994)). It is understood that one or more of the molecules of the invention, preferably one or more of the nucleic acid molecules or fragments thereof of the invention or one or more of the antibodies of the invention may be utilized to detect the level or pattern of a protein or mRNA thereof by *in situ* hybridization.

Fluorescent *in situ* hybridization allows the localization of a particular DNA sequence along a chromosome which is useful, among other uses, for gene mapping, following chromosomes in hybrid lines or detecting chromosomes with translocations, transversions or deletions. *In situ* hybridization has been used to identify chromosomes in several plant species (Griffor *et al., Plant Mol. Biol. 17*:101-109 (1991); Gustafson *et al., Proc. Natl. Acad. Sci. (U.S.A.) 87*:1899-1902 (1990); Mukai and Gill, *Genome 34*:448-452 (1991); Schwarzacher and Heslop-Harrison, *Genome 34*:317-323 (1991); Wang *et al., Jpn. J. Genet. 66*:313-316 (1991); Parra and Windle, *Nature Genetics 5*:17-21 (1993)). It is understood that the nucleic acid molecules of the invention may be used as probes or markers to localize sequences along a chromosome.

Another method to localize the expression of a molecule is tissue printing. Tissue printing provides a way to screen, at the same time on the same membrane many tissue sections from different plants or different developmental stages (Yomo and Taylor, *Planta 112*:35-43 (1973); Harris and Chrispeels, *Plant Physiol.* 56:292-299 (1975); Cassab and Varner, *J. Cell. Biol. 105*:2581-2588 (1987); Spruce *et al., Phytochemistry 26*:2901-2903 (1987); Barres *et al., Neuron 5*:527-544 (1990); Reid and Pont-Lezica, *Tissue Printing: Tools for the Study of Anatomy, Histochemistry and Gene Expression*, Academic Press, New York, New York (1992); Reid *et al., Plant Physiol. 93*:160-165 (1990); Ye *et al., Plant J. 1*:175-183 (1991)).

It is understood that one or more of the molecules of the invention, preferably one or more of the nucleic acid molecules of the present invention or one or more of the

antibodies of the invention may be utilized to detect the presence or quantity of a protein or fragment of the invention by tissue printing.

Further it is also understood that any of the nucleic acid molecules of the invention may be used as marker nucleic acids and or probes in connection with methods that require probes or marker nucleic acids. As used herein, a probe is an agent that is utilized to determine an attribute or feature (*e.g.* presence or absence, location, correlation, etc.) of a molecule, cell, tissue or plant. As used herein, a marker nucleic acid is a nucleic acid molecule that is utilized to determine an attribute or feature (*e.g.*, presence or absence, location, correlation, etc.) or a molecule, cell, tissue or plant.

This invention provides arrays of polynucleotide or peptide target molecules arranged on a surface of a substrate. The target molecules are preferably known molecules, *e.g.* polynucleotides (including oligonucleotides) or peptides, which are capable of hybridizing to complementary probes. The target molecules are preferably immobilized, *e.g.* by covalent or non-covalent bonding, to the surface in small amounts of substantially purified and isolated molecules in a grid pattern. By immobilized is meant that the target molecules maintain their position relative to the solid support under hybridization and washing conditions. Target molecules are deposited in small footprint, isolated quantities of "spotted elements" of preferably single-stranded polynucleotide preferably arranged in rectangular grids in a density of about 30 to 1000 or more spotted elements per square centimeter. The economics of arrays favors a high density design criteria providing microarrays for detection of transcription events for a large number of genes provided that the target molecules are sufficiently separated so that the intensity of the indicia of a binding event associated with highly expressed probe molecules does not overwhelm and mask the indicia of neighboring binding events. For high density microarrays each spotted element may contain up to about 50 or more copies of the target molecule, *e.g.* as few as about 4 to 10 strands of single-stranded cDNA on glass substrates or more cDNA on nylon substrates. Probe molecules are typically unknown molecules, often a mixture of unknown molecules, which are labeled, *e.g.* with a fluorescent, radioactive or enzymatic label. Preferably each copy of a probe molecule contains a label so that a measurement of label intensity is proportional to detected probe

concentration. Mixtures of probes from different sources can be differentially labeled, *e.g.* with different colored dyes or with different types of labels. For many applications a preferred label is a radioactive isotope nucleotide, *e.g.* a nucleotide such as dUTP, dCTP, dGTP or dATP with an isotope such as ^{32}P. An array "substrate" is typically a solid material for supporting target molecules; substrates can be flexible such as nylon membranes or rigid such as glass sheet or silicon wafer; nylon membranes are common, porous supports for microarrays.

Arrays of this invention can be prepared for use with classes or organisms, *e.g.* animals, plants or microorganisms. The arrays can be prepared from target molecules from a single species or multiple species. Exemplary single species arrays include animals such as human, mouse and *Drosophila*, plants such as maize, soybean, rice and *Arabidopsis thaliana* , microorganisms such as *Aspergillus nidulans*, *E. coli*, *Agrobacterium tumefaciens* and viruses. Useful arrays can also comprise target molecules from multiple species. Arrays with target molecules from single species can be used with probe molecules from the same species or a different species or a mixture or species, *e.g.* due to the ability of cross species homologous genes to hybridize. It is generally preferred for high stringency hybridization that the target and probe molecules be from the same species or even from a common tissue in an organism under study. However, because of homology, cross-species hybridization can be effective. In preferred aspects of this invention the organism of interest is a plant and the target molecules are selected from the nucleic acid molecules having at least 60 percent sequence identity to sequences in the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof. In other preferred aspects of the invention at least 10% of the target molecules on an array have at least 20 consecutive nucleotides of sequence which is at least 60%, more preferably up to 100%, identical with a sequence of the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or complements thereof.

Although the shape of the substrates can vary, it is common for the array to be disposed in a rectangular area on a planar surface of the substrate to facilitate registration of target molecules in an addressable array. Generally, the overall dimensions of an array are in the range of 1 to 40 cm. Target molecules can be immobilized on an array substrate by covalent or non-covalent binding. Examples of non-covalent binding include non-specific adsorption, non-specific binding through a specific binding pair member covalently attached to the support surface, and entrapment in a matrix material, *e.g.* a hydrated or dried separation medium, which presents the target in a manner sufficient for binding, *e.g.* hybridization, to occur. Examples of covalent binding include covalent bonds formed between the target and a functional group present on the surface of the solid support, *e.g.* –OH, where the functional group may be naturally occurring or present as a member of an introduced linking group.

Spotted elements can be placed on arrays by depositing target molecules in a grid pattern onto a substrate or fabricating oligonucleotide or peptide sequences *in situ* on a substrate. Array design and fabrication methods are well known in the art and disclosed for instance in U.S. Patents 4,923,901; 5,079,600; 5,143,854; 5,202,231; 5,242,974; 5,384,261; 5,405,783; 5,412,087; 5,424,186; 5,429,807; 5,436,327; 5,445,934; 5,472,672; 5,525,464; 5,527,681; 5,529,756; 5,532,128; 5,545,531; 5,554,501; 5,556,752; 5,561,071; 5,571,639; 5,593,839; 5,599,695; 5,624,711; 5,658,734; 5,700,637; 5,744,305; 5,800,992; 6,004,755 and 6,087,102.

Protocols for isolating nucleic acids, proteins and their fractions from cells, tissues, organs and whole organisms are described in: Maniatis *et al.*, *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Press)(1989); Scope R., *Protein Purification. Principle and Practice* (Springer-Verlag)(1994); and Deutscher, *Guide to Protein Purification* (Academic Press)(1990)). Such methods typically involve subjection of the original biological source to one or more of tissue/cell homogenization, nucleic acid/protein extraction, chromatography, centrifugation, affinity binding and the like.

The subject arrays or devices into which they are incorporated may conveniently be stored following fabrication for use at a later time. Under appropriate conditions, the subject arrays are capable of being stored for at least about 6 months and may be stored

for up to one year or longer. The subject arrays are generally stored at temperatures between about −20 °C. to room temperature, where the arrays are preferably sealed in a plastic container, *e.g.* bag, and shielded from light.

Such arrays are useful in a variety of applications, including gene discovery, genomic research and bioactive compound screening. One important use of arrays is in the analysis of differential gene expression, *e.g.* transcription profiling where the expression of genes in different cells, normally a cell of interest and a control, is compared and any discrepancies in expression are identified. In such assays, the presence of discrepancies indicates a difference in genes expressed in the cells being compared. Such information is useful for the identification of the types of genes expressed in a particular cell or tissue type in a known environment. Such gene expression analysis applications including differential expression analysis of diseased and normal tissue; different tissues or subtypes; tissues and cells under different condition states, like predisposition to disease, age, exposure to pathogens or toxic agents, etc.; and the like. Such applications generally involve the following steps: (a) preparation of probe, *e.g.* attaching a label to a plurality of expressed molecules; (b) contact of probe with the array under conditions sufficient for probe to bind with corresponding target, *e.g.* by hybridization or specific binding; (c) removal of unbound probe from the array; and (d) detection of bound probe. Each of these steps will be described in greater detail below.

Probe preparation depends on the specific nature of the probe, *e.g.* whether the probe is a polynucleotide or peptide. Polynucleotide probes may be RNA or DNA, as well as hybridizing analogues or mimetics thereof, *e.g.* nucleic acids in which the phosphodiester linkage has been replaced with a substitute linkage, such as a phosphorothioate, methylimino, methylphosphonate, phosphoramidite, guanidine and the like; and nucleic acids in which the ribose subunit has been substituted, *e.g.* hexose phosphodiester, peptide nucleic acids; and the like. The probe will have sufficient complementarity to its target to provide for the desired level of sequence specific hybridization. Polynucleotide probes can range from about 10 to 2000 nucleotides where short probes in the range of about 15 to 100 nucleotides are commonly called

oligonucleotide probes. Although polynucleotide probes may be double stranded, single stranded probes are preferred.

Peptide probes that find use in the subject invention include: antibodies, *e.g.* polyclonal, monoclonal, and binding fragments thereof; peptides with high affinity to the target, as well as analogues and mimetics thereof; ligands, receptors, and the like.

Generally, the probe molecule will be labeled to provide for detection in the detection step. By labeled is meant that the probe comprises a member of a signal producing system and is thus detectable, either directly or through combined action with one or more additional members of a signal producing system. Examples of directly detectable labels include isotopic and fluorescent materials incorporated into or covalently bonded to the probe molecule. More particularly the label can comprise a nucleotide monomeric unit, *e.g.* dNTP of a primer, or a photoactive or chemically active derivative of a detectable label which can be bound to a functional part of the probe molecule. Isotopic label elements include ^{32}P, ^{33}P, ^{35}S, ^{125}I, and the like. Fluorescent label elements include coumarin and its derivatives, *e.g.* 7-amino-4-methylcoumarin, aminocoumarin, bodipy dyes, such as Bodipy FL, cascade blue, fluorescein and its derivatives, *e.g.* fluorescein isothiocyanate, Oregon green, rhodamine dyes, *e.g.* Texas red, tetramethylrhodamine, eosins and erythrosins, cyanine dyes, *e.g.* Cy3 and Cy5, macrocyclic chelates of lanthanide ions, fluorescent energy transfer dyes, such as thiazole orange-ethidium heterodimer, TOTAB, etc. Labels may also be members of a signal producing system that act in concert with one or more additional members of the same system to provide a detectable signal. Illustrative of such labels are members of a specific binding pair, such as ligands, *e.g.* biotin, fluorescein, digoxigenin, antigen, polyvalent cations, chelator groups and the like, where the members specifically bind to additional members of the signal producing system, where the additional members provide a detectable signal either directly or indirectly, *e.g.* antibody conjugated to a fluorescent moiety or an enzymatic moiety capable of converting a substrate to a chromogenic product, *e.g.* alkaline phosphatase conjugate antibody; and the like. Additional labels of interest include those that provide for signal only when the probe with which they are associated is specifically bound to a target molecule, where such

labels include: "molecular beacons" as described in Tyagi & Kramer, Nature Biotechnology (1996) 14:303 and EP 0 070 685 B1. Other labels of interest include those described in U.S. Pat. No. 5,563,037; WO 97/17471 and WO 97/17076. A preferred label for polynucleotide probes is ^{32}P which is incorporated into copies of RNA via a radiolabeled dNTP, *e.g.* ^{32}P-dUTP.

Arrays of this invention preferably comprise at least 30 different and separated target nucleic acid molecules immobilized on a solid support in a manner that complementary probe nucleic acid molecules can be hybridized thereto, wherein said target nucleic acid molecules have at least 20 consecutive nucleotides in a sequence selected from the group consisting of:

(a) SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478;

(b) sequences which are complements of (a);

(c) sequences which have at least 60% identity to a sequence of (a) or (b);

(d) sequences of molecules of which hybridize to a sequence of (a) or (b) or (c);

Such arrays are useful in methods of this invention for determining a level or pattern of gene transcription in a plant cell or plant tissue under evaluation. Such methods comprise assaying the concentration of an mRNA molecule, whose concentration is dependent upon the transcription of said gene, by hybridizing the mRNA molecule to a second nucleic acid molecule according to this invention, *e.g.* molecules having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 and complements thereof. In a preferred method differences in rice, wheat, *Arabidopsis* or soy plant gene expression in at least two different plant tissues are analyzed by (a) obtaining a sample of ribonucleic acid molecules from each of the plant tissues; (b) generating from each sample of ribonucleic acid molecules a population of labeled nucleic acid molecules; (c) contacting each of populations of labeled nucleic acid molecules with a separate array of this invention; and (d) comparing the hybridization patterns thereof.

In such methods the array is contacted with probe molecules under conditions sufficient for binding between the probe and the target of the array. For example, where the probe and target are nucleic acids, the probe will be contacted with the array under conditions sufficient for hybridization to occur between the probe and target, where the hybridization conditions will be selected in order to provide for the desired level of hybridization specificity. For peptide probes, conditions will be selected to provide for specific binding between the probe and its target.

Contact of the array and probe involves contacting the array with an aqueous medium comprising the probe. Contact may be achieved in a variety of different ways depending on specific configuration of the array. For example, contact may be accomplished by simply placing the array in a container comprising the probe solution, such as a vial, plastic bag and the like. In other embodiments where the array is entrapped in a separation media bounded by two rigid plates, the opportunity exists to deliver the probe via electrophoretic means. Alternatively, where the array is incorporated into a biochip device having fluid entry and exit ports, the probe solution can be introduced into the chamber in which the pattern of target molecules is presented through the entry port, where fluid introduction could be performed manually or with an automated device. In multiwell embodiments, the probe solution will be introduced in the reaction chamber comprising the array, either manually, *e.g.* with a pipette, or with an automated fluid handling device. For flexible nylon substrate microarrays it is convenient to roll the nylon substrate into a roll for insertion into a vial where a small volume of probe solution can efficiently contact target through shaking.

Contact of the probe solution and the targets will be maintained for a sufficient period of time for binding between the probe and the target to occur. Although dependent on the nature of the probe and target, contact will generally be maintained for a period of time ranging from about 10 min to 24 hrs, usually from about 30 min to 12 hrs and more usually from about 1 hr to 6 hrs.

Following binding of probe and target, the resultant hybridization patterns of labeled probe may be visualized or detected in a variety of ways, with the particular manner of detection being chosen based on the particular label of the nucleic acid, where

representative detection means include scintillation counting, autoradiography, fluorescence measurement, calorimetric measurement, light emission measurement and the like. The method may or may not further comprise a non-bound label removal step prior to the detection step, depending on the particular label employed on the probe. For example, in homogenous assay formats a detectable signal is only generated upon specific binding of probe to target. As such, in homogenous assay formats, the hybridization pattern may be detected without a non-bound label removal step. In other embodiments, the label employed will generate a signal whether or not the probe is specifically bound to its is target. In such embodiments, the non-bound labeled probe is removed from the support surface. One means of removing the non-bound labeled probe is to perform the well known technique of washing, where a variety of wash solutions and protocols for their use in removing non-bound label are known to those of skill in the art and may be used. Alternatively, in those situations where the targets are entrapped in a separation medium in a format suitable for application of an electric field to the medium, the opportunity arises to remove non-bound labeled probe from the target by electrophoretic means. With radioactive labeled probes it is important to remove the unbound probe. The hybridization binding events can be read by exposure of a radioactive-labeled hybridized array to photographic film or preferably a digitizer for simultaneously reading and storing the intensity of the hybridization events.

The target expression level in the particular tissue being analyzed can be derived from the intensity of the detected signal. To ensure that an accurate level of expression is derived, it is useful to provide the array with standard spotted elements of blanks and fixed quantity of label to calibrate the detected probe signals.

Any of the nucleic acid molecules of the invention may either be modified by site directed mutagenesis or used as, for example, nucleic acid molecules that are used to target other nucleic acid molecules for modification.

It is understood that mutants with more than one altered nucleotide can be constructed using techniques that practitioners are familiar with, such as isolating restriction fragments and ligating such fragments into an expression vector (*see*, for

example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989)).

Two steps may be employed to characterize DNA-protein interactions. The first is to identify sequence fragments that interact with DNA-binding proteins, to titrate binding activity, to determine the specificity of binding and to determine whether a given DNA-binding activity can interact with related DNA sequences (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989)). Electrophoretic mobility-shift assay is a widely used assay. The assay provides a rapid and sensitive method for detecting DNA-binding proteins based on the observation that the mobility of a DNA fragment through a nondenaturing, low-ionic strength polyacrylamide gel is retarded upon association with a DNA-binding protein (Fried and Crother, *Nucleic Acids Res.* 9:6505-6525 (1981)). When one or more specific binding activities have been identified, the exact sequence of the DNA bound by the protein may be determined.

Several procedures for characterizing protein/DNA-binding sites are used (Maxam and Gilbert, *Methods Enzymol. 65*:499-560 (1980); Wissman and Hillen, *Methods Enzymol. 208*:365-379 (1991); Galas and Schmitz, *Nucleic Acids Res. 5*:3157-3170 (1978); Sigman *et al.*, *Methods Enzymol. 208*:414-433 (1991); Dixon *et al.*, *Methods Enzymol. 208*:414-433 (1991)). It is understood that one or more of the nucleic acid molecules of the invention may be utilized to identify a protein or fragment thereof that specifically binds to a nucleic acid molecule of the invention. It is also understood that one or more of the protein molecules or fragments thereof of the invention may be utilized to identify a nucleic acid molecule that specifically binds to it.

A two-hybrid system is based on the fact that proteins, such as transcription factors that interact (physically) with one another carry out many cellular functions. Two-hybrid systems have been used to probe the function of new proteins (Chien *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 88*:9578-9582 (1991); Durfee *et al.*, *Genes Dev. 7*:555-569 (1993); Choi *et al.*, *Cell 78*:499-512 (1994); Kranz *et al.*, *Genes Dev. 8*:313-327 (1994)).

Interaction mating techniques have facilitated a number of two-hybrid studies of protein-protein interaction. Interaction mating has been used to examine interactions

between small sets of tens of proteins (Finley and Brent, *Proc. Natl. Acad. Sci. (U.S.A.) 91*:12098-12984 (1994)), larger sets of hundreds of proteins (Bendixen *et al., Nucl. Acids Res. 22*:1778-1779 (1994)) and to comprehensively map proteins encoded by a small genome (Bartel *et al., Nature Genetics 12*:72-77 (1996)). This technique utilizes proteins fused to the DNA-binding domain and proteins fused to the activation domain. They are expressed in two different haploid yeast strains of opposite mating type and the strains are mated to determine if the two proteins interact. Mating occurs when haploid yeast strains come into contact and result in the fusion of the two haploids into a diploid yeast strain. An interaction can be determined by the activation of a two-hybrid reporter gene in the diploid strain.

It is understood that the protein-protein interactions of protein or fragments thereof of the invention may be investigated using the two-hybrid system and that any of the nucleic acid molecules of the invention that encode such proteins or fragments thereof may be used to transform yeast in the two-hybrid system.

(e) Computer Readable Media

The nucleotide sequence provided in SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 13478 or fragment thereof, or complement thereof, or a nucleotide sequence at least 70% identical, preferably 90% identical even more preferably 99% or about 100% identical to one or more of the nucleic acid sequences provided in SEQ ID NO: 1287 through SEQ ID NO:3291, SEQ ID NO: 5479 through SEQ ID NO: 8350, SEQ ID NO: 9242 through SEQ ID NO: 10474 SEQ ID 13478 or complement thereof or fragments of either or amino acid sequences provided in SEQ ID NO: 1 through SEQ ID NO 1286, SEQ ID NO: 3292 through SEQ ID NO: 5478, SEQ ID NO: 8351 through SEQ ID NO: 9241 and SEQ ID NO: 13479 through SEQ ID NO: 24143 or homologues thereof, can be "provided" in a variety of mediums to facilitate use.

In one application, a nucleotide or amino acid sequence of the invention can be recorded on computer readable media so that a computer–readable medium comprises one or more of the nucleotide or amino acid sequences of the invention. As used herein, "computer readable media" refers to any medium that can be read and accessed directly

by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc, storage medium and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

Any number of the sequences, or sequence fragments, of the nucleic acid molecules or proteins of the invention, or fragments of either, can be included, in any number of combinations, on a computer-readable medium.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the nucleic acid molecules or amino acid molecules of the present invention. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide or amino acid sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide or amino acid sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide or amino acid sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequence of the present invention that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for

conducting search means are available can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBI). One of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

The most preferred sequence length of a target sequence is from about 30 to 300 nucleotide residues or from about 10 to 100 of the corresponding amino acids. However, it is well recognized that during searches for commercially important fragments of the nucleic acid or amino acid molecules of the present invention may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, *cis* elements, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequences of the present invention sequence identified using a search means as described above, and an output means for outputting the identified homologous sequences. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the sequence of the present invention by varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

Computer media of the nucleic acid or amino acid sequences of this invention can comprise as few as 1000 distinct nucleic acid or amino acid sequences including complements and homologs, preferably at least 2,000 or 3,000, more preferably at least

5,000 or 10,000 or more, *e.g.* 15,000 or 20,000 and in certain embodiments as much as 30,00 or 40,000 distinct nucleic acid or amino acid sequences.

Having now described the invention, the following examples are provided by way of illustration and are not intended to limit the scope of the invention, unless specified.

Example 1

This example illustrates the construction of the rice genomic library. BACs are stable, non-chimeric cloning systems having genomic fragment inserts (100-300 kb) and their DNA can be prepared for most types of experiments including DNA sequencing. BAC vector, pBeloBAC11, is derived from the endogenous *E. coli* F-factor plasmid, which contains genes for strict copy number control and unidirectional origin of DNA replication. Additionally, pBeloBAC11 has three unique restriction enzyme sites (*Hind* III, *Bam* HI and *Sph* I) located within the *LacZ* gene which can be used as cloning sites for megabase-size plant DNA. Indigo, another BAC vector contains *Hind* III and *Eco* RI cloning sites. This vector also contains a random mutation in the *LacZ* gene that allows for darker blue colonies.

As an alternative, the P1-derived artificial chromosome (PAC) can be used as a large DNA fragment cloning vector (Ioannou *et al.*, *Nature Genet. 6*:84-89 (1994; Suzuki *et al.*, *Gene 199*:133-137 (1997). The PAC vector has most of the features of the BAC system, but also contains some of the elements of the bacteriophage P1 cloning system.

BAC libraries are generated by ligating size-selected restriction digested DNA with pBeloBAC11 followed by electroporation into *E. coli*. BAC library construction and characterization is extremely efficient when compared to YAC (yeast artificial chromosome) library construction and analysis, particularly because of the chimerism associated with YACs and difficulties associated with extracting YAC DNA.

There are general methods for preparing megabase-size DNA from plants. For example, the protoplast method yields megabase-size DNA of high quality with minimal breakage. The process involves preparing young leaves which are manually feathered with a razor-blade before being incubated for four to five hours with cell-wall-degrading enzymes. The second method developed by Zhange *et al.*, *Plant J. 7*:175-184 (1995) , is a universal nuclei method that works well for several divergent plant taxa. Fresh or

frozen tissue is homogenized with a blender or mortar and pestle. Nuclei are then isolated and embedded. DNA prepared by the nucleic method is often more concentrated and is reported to contain lower amounts of chloroplast DNA than the protoplast method.

Once protoplasts or nuclei are produced, they are embedded in an agarose matrix as plugs or microbeads. The agarose provides a support matrix to prevent shearing of the DNA while allowing enzymes and buffers to diffuse into the DNA. The DNA is purified and manipulated in the agarose and is stable for more than one year at 4°C.

Once high molecular weight DNA has been prepared, it is fragmented to the desired size range. In general, DNA fragmentation utilizes two general approaches, 1) physical shearing and 2) partial digestion with a restriction enzyme that cuts relatively frequently within the genome. Since physical shearing is not dependent upon the frequency and distribution of particular restriction enzymes sites, this method should yield the most random distribution of DNA fragments. However, the ends of the sheared DNA fragments must be repaired and cloned directly or restriction enzyme sites added by the addition of synthetic linkers. Because of the subsequent steps required to clone DNA fragmented by shearing, most protocols fragment DNA by partial restriction enzyme digestion. The advantage of partial restriction enzyme digestion is that no further enzymatic modification of the ends of the restriction fragments are necessary. Four common techniques that can be used to achieve reproducible partial digestion of megabase-size DNA are 1) varying the concentration of the restriction enzyme, 2) varying the time of incubation with the restriction enzyme 3) varying the concentration of an enzyme cofactor (*e.g.*, Mg^{2+}) and 4) varying the ratio of endonuclease to methylase.

There are three cloning sites in pBeloBAC11, but only *Hind* III and *Bam* HI produce 5' overhangs for easy vector dephosphorylation. These two restriction enzymes are primarily used to construct BAC libraries. The optimal partial digestion conditions for megabase-size DNA are determined by wide and narrow window digestions. To optimize the optimum amount of *Hind* III, 1, 2, 3, 10, and 5- units of enzyme are each added to 50 ml aliquots of microbeads and incubated at 37 °C for 20 minutes.

After partial digestion of megabase-size DNA, the DNA is run on a pulsed-field gel, and DNA in a size range of 100-500 kb is excised from the gel. This DNA is ligated

to the BAC vector or subjected to a second size selection on a pulsed field gel under different running conditions. Studies have previously reported that two rounds of size selection can eliminate small DNA fragments co-migrating with the selected range in the first pulse-field fractionation. Such a strategy results in an increase in insert sizes and a more uniform insert size distribution. A practical approach to performing size selections is to first test for the number of clones/microliter of ligation and insert size from the first size selected material. If the numbers are good (500 to 2000 white colony/microliter of ligation) and the size range is also good (50 to 300 kb) then a second size selection is practical. When performing a second size selection one expects a 80 to 95% decrease in the number of recombinant clones per transformation.

Twenty to two hundred nanograms of the size-selected DNA is ligated to dephosphorylated BAC vector (molar ratio of 10 to 1 in BAC vector excess). Most BAC libraries use a molar ratio of 5 to 15 : 1 (size selected DNA:BAC vector).

Transformation is carried out by electroporation and the transformation efficiency for BACs is about 40 to 1,500 transformants from one microliter of ligation product or 20 to 1000 transformants/ng DNA.

Several tests can be carried out to determine the quality of a BAC library. Three basic tests to evaluate the quality include: the genome coverage of a BAC library-average insert size, average number of clones hybridizing with single copy probes and chloroplast DNA content.

The determination of the average insert size of the library is assessed in two ways. First, during library construction every ligation is tested to determine the average insert size by assaying 20-50 BAC clones per ligation. DNA is isolated from recombinant clones using a standard mini preparation protocol, digested with *Not* I to free the insert from the BAC vector and then sized using pulsed field gel electrophoresis (Maule, *Molecular Biotechnology* 9:107-126 (1998)).

To determine the genome coverage of the library, it is screened with single copy RFLP markers distributed randomly across the genome by hybridization. Microtiter plates containing BAC clones are spotted onto Hybond membranes. Bacteria from 48 or 72 plates are spotted twice onto one membrane resulting in 18,000 to 27,648 unique

clones on each membrane in either a 4X4 or 5X5 orientation. Since each clone is present twice, false positives are easily eliminated and true positives are easily recognized and identified.

Finally, the chloroplast DNA content in the BAC library is estimated by hybridizing three chloroplast genes spaced evenly across the chloroplast genome to the library on high density hybridization filters.

There are strategies for isolating rare sequences within the genome. For example, higher plant genomes can range in size from 100 Mb/1C (*Arabidopsis*) to 15,966 Mb/C (*Triticum aestivum*), (Arumuganathan and Earle, *Plant Mol Bio Rep.9:*208-219 (1991)). The number of clones required to achieve a given probability that any DNA sequence will be represented in a genomic library is $N = (\ln(1-P))/(\ln(1-L/G))$ where N is the number of clones required, P is the probability desired to get the target sequence, L is the length of the average clone insert in base pairs and G is the haploid genome length in base pairs (Clarke *et al.*, *Cell* 9:91-100 (1976)).

The rice BAC library of the present invention is constructed in the pBeloBAC11 or similar vector. Inserts are generated by partial *Eco* RI or other enzymatic digestion of DNA.

Example 2

This example illustrates the construction of the *Arabidopsis thaliana* genomic library. DNA from *Arabidopsis thaliana, Landsberg erecta* seedlings is prepared by a CTAB genomic DNA isolation protocol as described by Dean *et al. Plant J 2*:69-81(1992) and modified by Dubois *et al. Plant J. 13*:141-151 (1998).

A solution of DNA to be sheared is prepared in a 1.5 ml microcentrifuge tube by mixing 15 ug of DNA, 6 µl of 10X mung bean (MB) buffer (10X MB buffer = 300mM NaOAc, pH 5.0, 500 mM NaCl, 10 mM $ZnCl_2$, 50% glycerol), and water to a final volume of 60 µl. The DNA solution is kept on ice prior to sonication. For sonication, a cup horn probe chilled with ice water for 1 hour prior to sonication is used. The sonicator (Ultrasonic Liquid Processor XL2020 , Misonix Inc.) is pulsed for approximately 10 seconds on full power prior to use. DNA samples are sonicated twice for 6 seconds each at 60% power. Four sample tubes may be processed at once in a multi-tube rack which is

positioned 1 to 3 mm above the opening in the probe. The DNA is returned to ice and a 1 μl sample is analyzed by electrophoresis on a 0.8% agarose gel in 0.5X TBE gel, run at 60 volts for 30 minutes. Sonication may be repeated if necessary.

A 0.26 μl aliquot of mung bean nuclease (150,000 u/ml) is added to sheared DNA and the sample is incubated at 30° C for 10 minutes. To stop the digestion, 20 μl of 1 M NaCl, 140 ul dd H_20, and 200 ml of phenol:chloroform are added to the sample which is then, vortexed and centrifuged for 20 minutes at 13,000 rpm. The resulting aqueous phase is transferred into a new 1.5 ml microcentrifuge tube, 500 μl of 95% ethanol is added, and the DNA is precipitated overnight at -80° C. The sample is centrifuged for 30 minutes at 13,000 rpm, washed with 500 μl of 95% ethanol and centrifuged again for 30 minutes at 13,000rpm. The sample is then dried under vacuum, and resuspended in 10 μl TE.

The sheared DNA fragments are sized and purified by preparative agarose gel electrophoresis. Five microliters of 6x BP-XC-glycerol dye (0.25% BP, 0.25% XC, 30% glycerol) is added to the sample. The sample is split into two samples and loaded (12.5 μl per lane) on a 0.8% (1x TAE) low-melting agarose gel (SeaPlaque GTG) and electrophoresed at 60 V, 46 mA for 3.5 hours.

The gel is photographed under long wave UV and slices containing DNA fragments of 1.3 - 1.7 kb and 2 - 4 kb are excised and excess agarose cut away. The gel slices are placed in 1.5 ml microcentrifuge tubes. One gel slice is stored at -20° C. 15 μl of 1 M NaCl is added to the other gel slice, followed by melting of the agarose by incubation at 65° C for 8 minutes. The resulting approximately 250 μl samples are placed into microcentrifuge tubes. An equal volume of water is added, following which the sample is vortexed and placed at room temperature for 2 minutes to bring the temperature up to 30 -35° C. 0.5 ml of water-saturated phenol that has been cooled on ice is added and the sample vortexed vigorously. The sample is placed on ice for 5 minutes, and the vortexing step repeated.

The sample is centrifuged at 4°C in a microcentrifuge for 20 minutes. The upper phase is transferred to a clean tube, and the bottom phenol layer is reextracted by addition of 200 μl of dd H2O. The sample is vortexed and placed on ice for 5 minutes, followed

by centrifugation for 15 minutes. The aqueous layer is extracted and added to the aqueous layer from the previous step. Phenol extraction is repeated with 0.5 ml phenol, followed by vortexing and centrifugation for 20 minutes at 4°C. The aqueous layer is removed and repeated sec-butanol extractions are performed until the final volume is reduced to approximately 0.165 ml

Two volumes of 95% ethanol (400 µl) are added and the sample is stored at -80° C overnight. The sample is centrifuged for 30 minutes at room temperature to pellet the DNA, washed once with 95% ethanol and dried briefly under vacuum. The sample is resuspended in 7 µl of TE. A 1 ul sample is run on a 0.8% agarose gel with markers to estimate concentration of recovered fraction.

M13 Library

20 ng of M13 DNA digested with *Sma*I is mixed with 1 µl of 10x ligation buffer (10X ligation buffer = 0.5M tris pH 7.4, 0.1M $MgCl_2$, 0.1M DDT), 1µl of 1mM ATP and 100 - 200 ng of sheared genomic DNA fragments (1 - 3 µl volume), and 0.3 µl of high concentration NEB ligase (5 unit/µl) is added. Water is added to a final volume of 10ul and the sample is incubated overnight at 14° C.

Plasmid Library

200 ng (4 µl) of pSTBlue vector (Novegene) is mixed with approximately 600 ng (12 µl) of sheared genomic DNA fragments from the 2-4kb size range gel slices and 1.2 µl of Gibco T4 ligase (5 units per µl) is added. Water is added to a final volume of 30ul and the sample is incubated overnight at 14° C.

Transformation

The ligation reaction is titered and diluted for optimal transformation efficiency. When the ligation contains approximately 20 ng of M13 vector, the dilution will typically be from 1:25 to 1:100. A 1:25 dilution is used for plasmid ligation containing approximately 200 ng of vector DNA. To increase transformation efficiency, the ligase is denatured by heating at 65°C for 7 minutes, and placed at room temperature for 5 minutes following the heating step.

A sterile electroporation cuvette is chilled for each transformation. Electro-competent cells are removed from the -80° C freezer and thawed on ice. For each M13

transformation, a sterile tube containing 25 ul of IPTG (25 mg/ml in water), 25 μl of X-Gal (25 mg/ml in dimethylformamide) and 3 ml of YT top agar is prepared, capped and placed in a 45° C water bath. YT plates are pre-warmed at 37° C for several hours to avoid cross-contamination problems that may result if water remains on plates. For plasmid transformations, a sterile tube containing 0.5 ml of SOC medium is prepared for each transformation, and L + amp plates are pre-spread with 25 μl of IPTG and 25 μl of X-Gal.

25 μl of electro-competent cells are mixed with DNA in diluted ligation mix in the cuvette, and the sample pulsed in an *E. coli* pulser (BioRad) set to the appropriate voltage (1.80kV for 0.1 cm cuvettes; 2.50kV for 0.2 cm cuvettes). The cuvette is removed from the pulser, and the sample immediately transferred to the tube containing SOC or YT top agar. For M13 transfections, the sample is plated immediately on YT plates. For plasmid transformations, the tube is placed in a 37° C shaker for 15-30 minutes and 30 ul aliquots are plated on L + Amp plates. Plates are incubated at 37° C overnight.

Example 3

This example serves to illustrate how the genomic sequences are sequenced and combined into contigs. Two basic methods can be used for DNA sequencing, the chain termination method of Sanger *et al.*, *Proc. Natl. Acad. Sci. USA 74:*5463-5467 (1977), the entirety of which is herein incorporated by reference and the chemical degradation method of Maxam and Gilbert, *Proc. Natl. Acad. Sci. USA 74:*560-564 (1977). Automation and advances in technology such as the replacement of radioisotopes with fluorescence-based sequencing have reduced the effort required to sequence DNA (Craxton, *Methods, 2:*20-26 (1991); Ju *et al.*, *Proc. Natl. Acad. Sci. USA 92:*4347-4351 (1995); Tabor and Richardson, *Proc. Natl. Acad. Sci. USA 92:*6339-6343 (1995)). Automated sequencers are available from, for example, Pharmacia Biotech, Inc., Piscataway, New Jersey (Pharmacia ALF), LI-COR, Inc., Lincoln, Nebraska (LI-COR 4,000) and Millipore, Bedford, Massachusetts (Millipore BaseStation).

In addition, advances in capillary gel electrophoresis have also reduced the effort required to sequence DNA and such advances provide a rapid high resolution approach

for sequencing DNA samples (Swerdlow and Gesteland, *Nucleic Acids Res. 18*:1415-1419 (1990); Smith, *Nature 349*:812-813 (1991); Luckey *et al.*, *Methods Enzymol. 218*:154-172 (1993); Lu *et al.*, *J. Chromatog. A. 680*:497-501 (1994); Carson *et al.*, *Anal. Chem. 65*:3219-3226 (1993); Huang *et al.*, *Anal. Chem. 64*:2149-2154 (1992); Kheterpal *et al.*, *Electrophoresis 17*:1852-1859 (1996); Quesada and Zhang, *Electrophoresis 17*:1841-1851 (1996); Baba, *Yakugaku Zasshi 117*:265-281 (1997)). The 3700 DNA Sequencer (Perkin-Elmer Corp., Applied Biosystems Div., Foster City, CA) is a machine which uses this technology.

A number of sequencing techniques are known in the art, including fluorescence-based sequencing methodologies. These methods have the detection, automation and instrumentation capability necessary for the analysis of large volumes of sequence data. With these types of automated systems, fluorescent dye-labeled sequence reaction products are detected and data entered directly into the computer, producing a chromatogram that is subsequently viewed, stored, and analyzed using the corresponding software programs. These methods are known to those of skill in the art and have been described and reviewed (Birren *et al., Genome Analysis: Analyzing DNA*,1, Cold Spring Harbor, New York (1999)).

PHRED is used to call the bases from the sequence trace files (www.mbt.washington.edu). Phred uses Fourier methods to examine the four base traces in the region surrounding each point in the data set in order to predict a series of evenly spaced predicted locations. That is, it determines where the peaks would be centered if there were no compressions, dropouts, or other factors shifting the peaks from their "true" locations. Next, PHRED examines each trace to find the centers of the actual, or observed peaks and the areas of these peaks relative to their neighbors. The peaks are detected independently along each of the four traces so many peaks overlap. A dynamic programming algorithm is used to match the observed peaks detected in the second step with the predicted peak locations found in the first step.

After the base calling is completed, contaminating sequences (*e.g.*, *E. coli*) are removed, and BAC vector and sub-cloning vectors sequence segments with > 30 bases

are trimmed and constraints are made for the assembler. Rice contigs are assembled using CAP3 (Huang *et al.*, *Genomics 46*: 37-45 (1997)).

A two-step re-assembly process is employed to reduce sequence redundancies caused by overlaps between BAC clones. In the first step, BAC clones are grouped into clusters based on overlaps between contig sequences from different BACs. These overlaps are identified by comparing each sequence in the dataset against every other sequences, by BLASTN. BACs containing overlaps greater than 5,000 base pairs in length and greater than 94% in sequence identity are put into the same cluster. Repetitive sequences are masked prior to this procedure to avoid false joining by repetitive elements present in the genome. In the second step, sequences from each BAC cluster are assembled by PHRAP.longread, which is able to handle very long sequences. A minimum match is set at 100 bp and a minimum score is set at 600 as a threshold to join input contigs into longer contigs.

Arabidopsis thaliana contigs are assembled using PANGEA clustering tools (PANGEA Systems, Inc.) and PHRAP (www.mbt.washington.edu). PANGEA clustering tools are a series of scripts which group sequences (clusters) by comparing pairs of sequences for overlapping bases. The overlap is determined using the following high stringency parameters: word size = 8; window size = 60; and identity is 93%. Each of the clusters are then assembled using PHRAP. This step results in islands. The next step is to combine the islands together to collapse the contig number even further. Default, less stringent parameters, are used in this step: minimum match =14, minimum score = 30; and the penalty is –2.

Example 4

This example illustrates the identification of genes within rice or *Arabidopsis thaliana* genomic contig libraries as assembled above. The genes and partial genes embedded in such contigs are identified through a series of informatic analyses. The tools to define genes fall into two categories: homology-based and predictive-based methods. Homology-based searches (*e.g.*, GAP2, BLASTX supplemented by NAP and TBLASTX) detect conserved sequences during comparisons of DNA sequences or hypothetically translated protein sequences to public and/or proprietary DNA and protein

databases. Existence of an *Oryza sativa* gene is inferred if significant sequence similarity extends over the majority of the target gene. Since homology-based methods may overlook genes unique to *Oryza sativa*, for which homologous nucleic acid molecules have not yet been identified in databases, gene prediction programs are also used. Predictive methods employed in the definition of the *Oryza sativa* genes include the use of the GenScan gene predictive software program. GeneScan is available from Stanford University (*e.g.* at the web site gnomic/stanford.edu/GENSCANW.html). In general terms, GenScan infers the presence and extent of a gene through a search for "gene-like" grammar.

The homology-based methods used to define the *Oryza sativa* gene set include BLASTX supplemented by NAP. For a description of BLASTX *see* Coulson, *Trends in Biotechnology* 12:76-80 (1994) and Birren *et al.*, *Genome Analysis,* 1:543-559 (1997). NAP is part of the Analysis and Annotation Tool (AAT) for Finding Genes in Genomic Sequences which was developed by Xiaoqiu Huang at Michigan Tech University and is available at the web site genome.cs.mtu.edu/. The AAT package includes two sets of programs, one set DPS/NAP (referred to as "NAP") for comparing the query sequence with a protein database, and the other set DDS/GAP2 (referred to as "GAP2") for comparing the query sequence with a cDNA database. Each set contains a fast database search program and a rigorous alignment program. The database search program quickly identifies regions of the query sequence that are similar to a database sequence. Then the alignment program constructs an optimal alignment for each region and the database sequence. The alignment program also reports the coordinates of exons in the query sequence. *See* Huang *et al., Genomics 46*: 37-45 (1997).

The NAP program computes a global alignment of a DNA sequence and a protein sequence without penalizing terminal gaps. NAP handles frameshifts and long introns in the DNA sequence. The program delivers the alignment in linear space, so long sequences can be aligned. It makes use of splice site consensuses in alignment computation. Both strands of the DNA sequence are compared with the protein sequence and one of the two alignments with the larger score is reported. *See* Huang, and Zhang, "*Computer Applications in the Biosciences* 12(6), 497-506 (1996).

NAP takes a nucleotide sequence, translates it in three forward reading frames and three reverse complement reading frames, and then compares the six translations against a protein sequence database (*e.g.* the non-redundant protein (*i.e.*, nr-aa) database maintained by the National Center for Biotechnology Information as part of GenBank and available at the web site: www.ncbi.nlm.nih.gov).

The second homology-based method used for gene discovery is BLASTX hits extended with the NAP software package. BLASTX is run with the *Oryza sativa* genomic contigs as queries against the GenBank non-redundant protein data library identified as "nr.aa". NAP is used to better align the amino acid sequences as compared to the genomic sequence. NAP extends the match in regions where BLASTX has identified high-scoring-pairs (HSPs), predicts introns, and then links the exons into a single ORF prediction. Experience suggests that NAP tends to mis-predict the first exon. The NAP parameters are:

gap extension penalty = 1
gap open penalty = 15
gap length for constant penalty = 25
min exon length (in aa) = 7
minimum total length of all exons in a gene (in nucleotide) = 200
homology > 40%

The NAP alignment score and GenBank reference number for best match are reported for each contig for which there is a NAP hit.

The GenScan program is "trained" with *Arabidopsis thaliana* characteristics. Though better than the "off-the-shelf" version, the GenScan trained to identify *Oryza sativa* and *Arabidopsis thaliana* genes proved more proficient at predicting exons than predicting full-length genes. Predicting full-length genes is compromised by point mutations in the unfinished contigs, as well as by the short length of the contigs relative to the typical length of a gene. Due to the errors found in the full-length gene predictions by GenScan, inclusion of GenScan-predicted genes is limited to those genes and exons whose probabilities are above a conservative probability threshold. The GenScan parameters are:

weighted mean GenScan P value > 0.4

mean GenScan T value > 0

mean GenScan Coding score > 50

length > 200 bp

The weighted mean GenScan P value is a probability for correctly predicting ORFs or partial ORFs and is defined as the $(1/\Sigma\, l_i)(\Sigma\, l_i\, P_i)$, where "l" is the length of a exon and "P" is the probability or correctness for the exon.

Example 5

This example illustrates the generation of the EST libraries from cDNA prepared from a variety of *Arabidopsis thaliana*, Columbia ecotype, *Glycine max*, *Oryza sativa* and *Zea mays* tissue. Wild type *Arabidopsis thaliana* seeds are planted in commonly used planting pots and grown in an environmental chamber. Tissue is harvested as follows:

(a) For leaf tissue-based cDNA, leaf blades are cut with sharp scissors at seven weeks after planting;

(b) For root tissue-based cDNA, roots of seven-week old plants are rinsed intensively with tap water to wash away dirt, and briefly blotted by paper towel to take away free water;

(c) For stem tissue-based cDNA, stems are collected seven to eight weeks after planting by cutting the stems from the base and cutting the top of the plant to remove the floral tissue;

(d) For flower bud tissue-based cDNA, green and unopened flower buds are harvested about seven weeks after planting;

(e) For open flower tissue-based cDNA, completely opened flowers with all parts of floral structure observable, but no siliques are appearing, and are harvested about seven weeks after planting;

(f) For immature seed tissue-based cDNA, seeds are harvested at approximately 7-8 weeks of age. The seeds range in maturity from the smallest seeds that could be dissected from siliques to just before starting to turn yellow in color.

All tissue is immediately frozen in liquid nitrogen and stored at -80 °C until total RNA extraction. The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The cDNA libraries are plated on LB agar containing the appropriate antibiotics for selection and incubated at 37° for a sufficient time to allow the growth of individual colonies. Single colonies are individually placed in each well of a 96-well microtiter plates containing LB liquid including the selective antibiotics. The plates are incubated overnight at approximately 37°C with gentle shaking to promote growth of the cultures. The plasmid DNA is isolated from each clone using Qiaprep plasmid isolation kits, using the conditions recommended by the manufacturer (Qiagen Inc., Santa Clara, California U.S.A.).

The template plasmid DNA clones are used for subsequent sequencing. For sequencing the cDNA libraries, a commercially available sequencing kit, such as the ABI PRISM dRhodamine Terminator Cycle Sequencing Ready Reaction Kit with AmpliTaq® DNA Polymerase, FS, is used under the conditions recommended by the manufacturer (PE Applied Biosystems, Foster City, CA). The ESTs of the present invention are generated by sequencing initiated from the 5' end of each cDNA clone.

A number of sequencing techniques are known in the art, including fluorescence-based sequencing methodologies. These methods have the detection, automation and instrumentation capability necessary for the analysis of large volumes of sequence data. Currently, the 377 DNA Sequencer (Perkin-Elmer Corp., Applied Biosystems Div., Foster City, CA) allows the most rapid electrophoresis and data collection. With these

types of automated systems, fluorescent dye-labeled sequence reaction products are detected and data entered directly into the computer, producing a chromatogram that is subsequently viewed, stored, and analyzed using the corresponding software programs. These methods are known to those of skill in the art and have been described and reviewed (Birren *et al.*, *Genome Analysis: Analyzing DNA*,1, Cold Spring Harbor, New York).

The generated ESTs (including any full length cDNA sequences) are combined with ESTs and full length cDNA sequences in public databases such as GenBank. Duplicate sequences are removed; and duplicate sequence identification numbers are replaced. The combined dataset is then clustered and assembled using Pangea Systems tool identified as CAT v.3.2. First, the EST sequences are screened and filtered, *e.g.* high frequency words are masked to prevent spurious clustering; sequence common to known contaminants such as cloning bacteria are masked; high frequency repeated sequences and simple sequences are masked; unmasked sequences of less than 100 bp are eliminated. The thus-screened and filtered ESTs are combined and subjected to a word-based clustering algorithm which calculates sequence pair distances based on word frequencies and uses a single linkage method to group like sequences into clusters of more than one sequence, as appropriate. Clustered sequence files are assembled individually using an iterative method based on PHRAP/CRAW/MAP providing one or more self-consistent consensus sequences and inconsistent singleton sequences. The assembled clustered sequence files are checked for completeness and parsed to create data representing each consensus contiguous sequence (contig), the initial EST sequences, and the relative position of each EST in a respective contig. The sequence of the 5' most clone is identified from each contig. The initial sequences that are not included in a contig are separated out. A FASTA file is created consisting of sequences comprising the sequence of each contig and all original sequences which were not included in a contig.

Example 6

cDNA sequences are assembled as above and are translated into all six reading frames. Translations of genes or gene fragments from genomic DNA whose coordinates are determined by Genscan or AAT/NAP are searched against standard or fragment Pfam

(version 5.3) profile Hidden Markov Models for transcription factor families as are the cDNA translations (A. Bateman, E. Birney, R. Durbin, S.R. Eddy, K.L. Howe, and E.L.L. Sonnhammer *Nucleic Acids Research*, 28:263-266, 2000). HMMs for transcription factor families in Pfam were rebuilt using HMMER software based on the full alignment provided in Pfam. The E value cutoff is set at 10.

Hidden Markov Models are constructed for transcription factor families not included in the Pfam database by aligning known domains manually. Hidden Markov Models are built using hmmbuild (with and without the –f option) using the HMMER software with the alignments as input. HMM models are calibrated using the HMMER software (hmmcalibrate) with the HMM model as input. Protein data sets are searched with the HMM models using hmmsearch in the HMMER software package version 2.1.1 using default parameters.

Framealign searches are used when known transcription factor domains are not detected by Hidden Markov Models. In these cases, the domains per transcription factor family are listed from the Transfac database (Wingender, E., Chen, X., Hehl, R., Karas, H., Liebich, I., Matys, V., Meinhardt, T., Prüß, M., Reuter, I. and Schacherer, F.:TRANSFAC: an integrated system for gene expression regulation *Nucleic Acids Res. 28*, 316-319 (2000)). Using Gencore software version 4.5.4 (Compugen, www.cgen.com) DNA datasets are framealign searched with each domain using an E value cutoff of 1E-3 all other parameters are default. The search results are combined for all domains per family.

Additional transcription factors are found by keyword searches which are carried out against cDNA sequences annotated using the BLAST 2.0 suite of programs with default parameters. Keyword searching is carried out against the top hit (E value better than or equal to 1E-08) using terms indicative of transcription factor families from Table 1.

Description of the Tables:

Table 1 Column Headings:

Transcription Factor Family: Entries in this column list the transcription factor families as listed in the Pfam database (pfam.wustl.edu/), Transfac (Wingender, E., *et al.*, *Nucleic Acids Res. 28*, 316-319 (2000) or PROSITE (expasy.proteome.org.au/prosite/).

Family Description: Entries in this column describe the transcription factor families listed in column 1. These descriptions are from the Pfam database (pfam.wustl.edu/), Transfac (Wingender, E., *et al.*, *Nucleic Acids Res. 28*, 316-319 (2000) or PROSITE (expasy.proteome.org.au/prosite/).

Related families: Entries in this column list the transcription factor families related to the families listed in column 1.

Table 2

Table 2 lists the *Arabidopsis thaliana* amino acid sequences translated from cDNA sequences determined to be transcription factors as analyzed in Example 6, above.

Table 2 column headings

SEQ NUM

The entries in the SEQ NUM column refer to the corresponding sequence in the sequence listing

SEQ ID

The SEQ ID is the name of the sequence as given in the SEQDB database (Monsanto, St. Louis Missouri). ".f1",".f2",".f3",".f4",".f5" and ".f6" refer the frame in which these sequences are translated from their corresponding nucleic acid sequence listed in Table 3.

Family/Method/E value

Entries in this column list the transcription factor family to which the sequence belongs. The families are described in Table 1. The entries also list the method used to determine transcription factor family. "HMM" refers to the Hidden Markov Model method as described in Example 6. "Framesearch" refers to the framealign search method described in Example 6 and "keyword" refers to BLAST annotation followed by keyword searching as described in Example 6.

The E value for each of the methods is also listed in this column. E value is defined as the expectation E (range 0 to infinity) calculated for an alignment between the query sequence and a database sequence can be extrapolated to an expectation over the entire database search, by converting the pairwise expectation to a probability (range 0-1) and multiplying the result by the ratio of the entire database size (expressed in residues) to the length of the matching database sequence. In detail:

$$E\_database = (1 - \exp(-E))\, D / d$$

where D is the size of the database; d is the length of the matching database sequence; and the quantity (1 - exp(-E)) is the probability, P, corresponding to the expectation E for the pairwise sequence comparison.

Table 3

Table 3 lists the sequences encoding transcription factors for *Arabidopsis thaliana*. These nucleic acid molecules are cDNA sequences assembled as in Example 6. They encode the amino acid molecules listed in Table 2. Correspondence between a particular nucleic acid molecule and its amino acid sequence is evident in that both have the same names under the Seq ID column except that the amino acid sequences in Table 2 are followed by .f1,.f2,.f3,.f4,.f5,f6 referring to the frame in which they are translated.

The column heading descriptions are the same as in Table 2.

Table 4

Table 4 lists the amino acid sequences determined to be transcription factors from maize. ".f1",".f2",".f3",".f4",".f5" and ".f6" extensions under the Seq ID column refer the frame in which these sequences are translated from their corresponding nucleic acid sequence listed in Table 5. The column headings are the same as in Table 2.

Table 5

Table 5 lists the sequences encoding transcription factors for maize. These nucleic acid molecules are cDNA sequences assembled as in Example 6. They encode the amino acid molecules listed in Table 4. Correspondence between a particular nucleic acid molecule and its amino acid sequence is evident in that both have the same names under the Seq ID column except that the amino acid sequences in Table 5 are followed by .f1,.f2,.f3,.f4,.f5,f6 referring to the frame in which they are translated.

The column heading descriptions are the same as in Table 2.

Table 6

Table 6 lists the amino acid sequences determined to be transcription factors from rice. ".frame1",".frame2",".frame3",".frame4",".frame5" and ".frame6" extensions under the Seq ID column refer the frame in which these sequences are translated from their corresponding nucleic acid sequence listed in Table 7. The column headings are the same as in Table 2.

Table 7

Table 7 lists the sequences encoding transcription factors for rice. These nucleic acid molecules are cDNA sequences assembled as in Example 5. They encode the amino acid molecules listed in Table 6. Correspondence between a particular nucleic acid molecule and its amino acid sequence is evident in that both have the same names under the Seq ID column except that the amino acid sequences in Table 6 are followed by .f1,.f2,.f3,.f4,.f5,f6 referring to the frame in which they are translated.

The column heading descriptions are the same as in Table 2.

Table 8

Table 8 lists the amino acid sequences determined to be transcription factors from soy. ".f1",".f2",".f3",".f4",".f5" and ".f6" extensions under the Seq ID column refer the frame in which these sequences are translated from their corresponding nucleic acid sequence listed in Table 9. The column headings are the same as in Table 2.

Table 9

Table 9 lists the sequences encoding transcription factors for rice. These nucleic acid molecules are cDNA sequences assembled as in Example 6. They encode the amino acid molecules listed in Table 8. Correspondence between a particular nucleic acid molecule and its amino acid sequence is evident in that both have the same names under the Seq ID column except that the amino acid sequences in Table 8 are followed by .f1,.f2,.f3,.f4,.f5,f6 referring to the frame in which they are translated.

The column heading descriptions are the same as in Table 2.

Table 10

Table 10 lists *Arabidopsis thaliana* amino acid sequences determined to be transcription factors by the methods in Example 6. These amino acid sequences are translated from genomic DNA sequences. The translation coordinates are determined by GENSCAN as described in Example 4.

The column heading descriptions are the same as in Table 2

Table 11

Table 11 lists rice amino acid sequences determined to be transcription factors by the methods in Example 6. These amino acid sequences are translated from genomic DNA sequences. The translation coordinates are determined by GENSCAN as described in Example 4.

The column heading descriptions are the same as in Table 2.

Table 12

Table 12 lists rice amino acid sequences determined to be transcription factors by the methods in Example 6. These amino acid sequences are translated from genomic DNA sequences. The translation coordinates are determined by AAT/NAP as described in Example 4.

The column heading descriptions are the same as in Table 2.

All references, patents, and patent applications cited in this application are incorporated by reference in their entirety.

Table 1

Transcription factor family	Family description	Related families
AP2	This 60 amino acid residue domain can bind to DNA -- this domain is plant specific -- members of this family are suggested to be related to pyridoxal phosphate-binding domains such as found in aminotran 2 – ethylene response (inducible). Examples: ethylene-responsive element binding proteins (EREBPs) & *E. coli* universal stress protein UspA	
ANK	Ankyrin repeat. Some Ankyrin-only proteins will interact with rel-ankyrin proteins to inhibit DNA binding activity. Examples: IkB α, γ, β and cactus.	
ARF	Auxin response factor -- plant specific. Not in Pfam– not to be confused with similarly named ADP-ribosylation factor (GTP binding protein) which is listed as ARF in Pfam.	
ARID	AT-Rich Interaction Domain – DNA-binding. Examples: Structural homology with T4 RNase H, *E. coli* endonuclease III & *Bacillus subtilis* DNA polymerase I	
AT-hook	The AT-hook is an AT-rich DNA-binding motif that was first described in mammalian high-mobility-group non-histone chromosomal protein HMG-I/Y. It is necessary and sufficient for binding to the narrow minor groove of stretches of AT-rich DNA via a conserved nine amino acid peptide (KRPRGRPKK). Many of the AT-hook DNA-binding motif proteins have been shown to have an effect on the structure and architecture of chromatin at levels beyond the action of the basic histones. They have been shown to also play a role in transcription regulation by acting as cofactors.	
14-3-3	The 14-3-3 proteins are a family of closely related acidic homodimeric proteins of about 30 Kd. The GF14 (G-Box Factor 14-3-3 Homolog) family are a group of proteins similar to 14-3-3 proteins that bind G-box oligonucleotides in promoters to regulate transcription.	
B3	Similar to ARF – plant specific. Not in Pfam. Binds DNA directly.	
BAH	Bromo-adjacent homology. Appears to act as a protein-protein interaction module specialized in gene silencing. It might play an important role by linking DNA methylation, replication and transcriptional regulation. Examples: DNA (cytosine-5) methyltransferases & Origin recognition complex 1 (Orc1) proteins.	bromodomain
basic	This basic domain is found in the MyoD family of muscle specific proteins that control muscle development. The bHLH region of the MyoD family includes the basic domain and the Helix-loop-helix (HLH) motif. The bHLH region mediates specific DNA binding with 12 residues of the basic domain involved in DNA binding. The basic domain forms an extended alpha helix in the structure.	bHLH
BPF-1	The parsley BPF-1 protein (Box P-binding factor) was identified as a transcription factor that bound the promoter of	

	phenylalanine ammonia lyase (PAL1) in response to a fungal elicitor. An Arabidopsis homolog HPPBF-1 (H-protein promoter binding factor-1), was found to regulate light-dependent expression of the H subunit of glycine decarboxylase, a mitochondrial enzyme complex involved in photorespiration.	
bromodomain	About 70 amino acids -- Exact function of this domain is not yet known but it is thought to be involved in protein-protein interactions and it may be important for the assembly or activity of multicomponent complexes involved in transcriptional activation. Examples: Mammalian CREB-binding protein; also found in many chromatin associated proteins -- bromodomains can interact specifically with acetylated lysine.	BAH
BTB	Named for BR-C, ttk and bab -- approximately 115 amino acids. The POZ or BTB domain is also known as BR-C/Ttk or ZiN Found primarily in zinc finger proteins -- present near the N-terminus of a fraction of zinc finger (zf-C2H2) proteins. The BTB/POZ domain mediates homomeric dimerization and in some instances heteromeric dimerization -- inhibits the interaction of their associated finger regions with DNA -- shown to mediate transcriptional repression and to interact with components of histone deacetylase co-repressor complexes. Other Examples: *Drosophila* bric a brac protein plus an estimated 40 members in *Drosophila*.	POZ Zf-C2H2
BZIP	Basic region mediating sequence-specific DNA-binding followed by a leucine zipper required for dimerization -- family is quite large. Examples: Fos, Jun, CRE, & *Arabidopsis* G-box binding factors GBF.	
CBFD, NFYB, HMF	Histone-like transcription factors (CBF/NF-Y) and archaeal histones CCAAT-binding factor (CBF). Heteromeric transcription factor that consists of two different components, both needed for DNA-binding. First subunit of CBFD (NF-YB) binds DNA (protein of 116 to 210 amino-acid residues); the second subunit of CBFD (NF-YA) contains an N-terminal subunit-association domain and a C-terminal DNA recognition domain (a protein of 265 to 350 amino-acid residues). Other Examples: histone-like subunits of transcription factor IID.	Histones
chromo	CHRromatin Organization MOdifier -- about 60 amino acids Originally found in proteins that modify the structure of chromatin to the condensed morphology of heterochromatin (Drosophila modifiers of variegation). Examples: Fission yeast swi6 (repression of the silent mating-type loci mat2 and mat3), *Drosophila* protein Su(var)3-9 (a suppressor of position-effect variegation), & mammalian DNA-binding/helicase proteins CHD-1 to CHD-4.	chromo shadow

chromo shadow	This domain is distantly related to chromo. This domain is always found in association with a chromo domain although not all chromo domain proteins contain the chromo shadow. Examples: Fission yeast swi6 (repression of the silent mating-type loci mat2 and mat3).	chromo
Copper-fist	Some fungal transcription factors contain a N-terminal domain which seems to be involved in copper-dependent DNA-binding -- undergo a conformational change in presence of copper. Examples: Yeast ACE1 (or CUP2) and *Candida glabrata* AMT1 which regulate the expression of the metallothionein genes -- *Yarrowia lipolytica* copper resistance protein CRF1.	
CSD	Cold shock domain -- about 70 amino acids. Binds to the CCAAT-containing Y box and the B box. Binds to cold tolerance gene promoters in bacteria. Examples: *E. coli* protein CS7.4 (gene cspA) which is induced in response to low temperature & *Bacillus subtilis* cold-shock proteins cspB and cspC.	
Ctf/nf1	Nuclear factor I (NF-I) or CCAAT box-binding transcription factor (CTF) (also known as TGGCA-binding proteins) are a family of vertebrate nuclear proteins which recognize and bind, as dimers, the palindromic DNA sequence 5'-TGGCANNNTGCCA-3'. CTF/NF-I binding sites are present in viral and cellular promoters and in the origin of DNA replication of Adenovirus type 2.	
Dm-domain	The DM domain is named after dsx and mab-3 -- dsx contains a single amino-terminal DM domain, whereas mab-3 contains two amino-terminal domains. The DM domain has a pattern of conserved zinc chelating residues C2H2C4. The dsx DM domain has been shown to dimerize and bind palindromic DNA.	
Dof	Dof proteins are a family of TFs that share a unique DNA-binding domain of ~52 aa. May form a single zinc-finger that is essential for DNA recognition. Plant specific and have various roles in the cell. Found in both monocots and dicots.	
DPB	Described by Mendel as the DNA-binding protein (DBP) family, a collection of miscellaneous proteins that have been functionally identified by their ability to physically bind to DNA via a DNA-binding domain. Here, includes the remorin like DNA-binding proteins. Also see TEO which describes the PCF1/2 like TFs.	TEO
ENBP	ENBP1 (early nodulin gene-binding protein 1), binds to an AT-rich regulatory element of psENOD12b to regulate its expression upon infection of plant root hairs by nitrogen-fixing bacteria. ENBP1 and ENBP1-like transcription factors are probably involved in general cellular processes, others than in a symbiotic context.	
Ets	Ets transcription factors are nuclear effectors of the Ras-MAP-kinase signaling pathway. Avian leukemia virus E26 is a replication defective retrovirus that induces a mixed erythroid/myeloid leukemia in chickens. E26 virus carries two distinct oncogenes, v-myb and v-ets. The ets portion of this oncogene is required for the induction of erythroblastosis. V-ets and c-ets-1, its cellular progenitor, have	

	been shown to be nuclear DNA-binding proteins.	
Fork_head	About 100 amino-acid residues, also known as the "winged helix" – present in some eukaryotic trasncription factors – involved in DNA-binding. Examples: *Drosophila* forkhead (fkh), mammalian transcriptional activators HNF-3-alpha, -beta, and –gamma, human HTLF, Xenopus XFKH1, yeast HCM1, yeast FKH1.	
GATA	GATA family of transcription factors are proteins that bind to DNA sites with the consensus sequence (A/T)GATA(A/G). Contain a pair of highly similar 'zinc finger' type domains. Examples: GATA 1-4 are TF found in mammals; they regulate development in certain cell types by binding to the GATA promoter region of globulin genes, & others. Note: A similar single 'zinc finger' domain protein is involved in positive and negative nitrogen metabolism gene regulation in fungus and yeast and also *Neurospora crassa* light regulated genes.	Zinc Finger
Gld	A domain with limited amino acid similarity to the TEA DNA binding domain found in a number of regulatory genes from fungi, insects, and mammals. This domain is predicted to form two alpha helices with sequence similarity to two alpha helices of the TEA domain that are implicated in DNA binding. These proteins are not picked up by Pfam's TEA model. Found in some response_reg proteins. Examples: ARR, AT1; both in Arabidopsis. Golden2 in maize.	Response_reg
HhH	Helix-hairpin-helix motif – multiple domains found in a protein. These HhH motifs bind DNA in a non-sequence-specific manner. Examples: Rat pol beta, endonuclease III, AlkA, & the 5' nuclease domain of *Taq* pol I.	
Hist_deacetyl	Regulation of transcription is caused in part by reversibly acetylating histones on several lysine residues. Histone deacetylases catalyze the removal of the acetyl group.	
HLH	Helix-loop-helix domain – 40 to 50 amino acid residues. Two amphipathic helices joined by a variable length linker region that could form a loop. This 'helix-loop-helix' (HLH) domain mediates protein dimerization -- most of these proteins have an extra basic region of about 15 amino acid residues adjacent to the HLH domain which specifically binds to DNA – members of the family are referred to as basic helix-loop-helix proteins (bHLH) -- bind E boxes -- dimerization is necessary but independent of DNA binding -- proteins without basic region act as repressors since they are unable to bind DNA but do dimerize. Examples: Myc (oncogene), Myo (muscle differentiation), Maize anthocyanin regulatory proteins, and other cellular differentiation TFs.	bHLH
HMG_box	High mobility group; relatively low molecular weight non-histone components in chromatin Known to bind to nucleosomes in active chromatin – thought to be invovled in chromatin formation.	
HMG14_17	High mobility group.	HMG

	HMG14 and HMG17 are two related proteins of about 100 amino acid residues that bind to the inner side of the nucleosomal DNA thus altering the interaction between the DNA and the histone octamer. These two proteins may be involved in the process that maintains transcribable genes in a unique chromatin conformation.	
Homeobox	Master control homeotic genes which determine body plan -- 60-residue motif – subfamilies named for 3 *Drosophila* gene families. Play an important role in development - most are known to be sequence-specific DNA-binding transcription factors. The domain binds DNA through a helix-turn-helix (HTH) structure. -- Homeobox is a 3-element fingerprint that provides a signature for the homeobox domain of homeotic proteins. Examples: *Drosophila* hox proteins: antennapedia (Antp), abdominal-A (abd-A), deformed (Dfd), proboscipedia (pb), sex combs reduced (scr), and ultrabithorax (ubx) which are collectively known as the 'antennapedia' subfamily; the engrailed subfamily defined by engrailed (en) which specifies the body segmentation pattern and is required for the development of the CNS; and the paired gene subfamily.	Pou
Histone	Histone protein is unique to eukaryotes -- an octamer is assembled to form chromatin with 146 base pairs of DNA organized into a superhelix around a histone octomer to create a nucleosome ('beads on a string'). Examples: H2A, H2B, H3, & H4.	Linker histone
HSF_DNA-binding	Heat shock factor (HSF) is a DNA-binding protein that specifically binds heat shock promoter elements (HSE). HSF is expressed at normal temperatures but is activated by heat shock or chemical stresses.	
IAA	The Aux/IAA proteins were identified as a class of short-lived, nuclear localized proteins that are rapidly transcriptionally induced in response to auxin . These proteins contain four highly conserved domains (boxes I, II, III, IV)- this model covers boxes III and IV. See ARF family in this document for related proteins.	ARF
IBR	The IBR (In Between Ring fingers) domain is found to occur between pairs of ring fingers (Zf-C3HC4). The function of this domain is unknown.	Zf-C3HC4
irf	This family of transcription factors are important in the regulation of interferons in response to infection by virus and in the regulation of interferon-inducible genes. Three of the five conserved tryptophan residues bind to DNA.	
K-box	K-box region is commonly found associated with SRF-type transcription factors. The K-box is a possible coiled-coil structure. Possible role in multimer formation. Examples: PISTILLATA (PI) gene of *Arabidopsis* causes homeotic conversion of petals to sepals and of stamens to carpels & SRF (Serum response factor) binds the serum response element.	SRF-TF/MADS
KRAB	The KRAB domain (or Kruppel-associated box) is present in about a third of zinc finger proteins containing C2H2 fingers. The KRAB domain is found to be involved in protein-protein	Zinc Finger proteins

	interactions.	
LIM	Cysteine-rich domain of about 60 amino-acid residues. Generally occurs as two tandem copies in proteins – in the LIM domain, there are seven conserved cysteine residues and a histidine -- the LIM domain binds two zinc ions -- LIM does not bind DNA, rather it seems to act as interface for protein-protein interaction. Examples: Pollen specific protein (SF3), Mammallian zinc absorption protein, Vertebrate paxillin (cytoskeletal focal adhesion protein), Plaque adhesion protein, and several homeotic proteins.	Homeobox Zinc-finger
Linker_histone	Member of histone octamer – see histone. Examples: H1, H5	Histone
MADS	See SRF-TF	
Myb_DNA-binding	This family contains the DNA-binding domains from the Myb proteins, as well as the SANT domain family. Retroviral oncogene v-myb, and its cellular counterpart c-myb, encode nuclear DNA-binding proteins that specifically recognize the sequence YAAC(G/T)G. Examples: Maize C1 protein (anthocyanin biosynthesis), Maize P protein (regulates the biosynthetic pathway of a flavonoid-derived pigment in certain floral tissues), *Arabidopsis* GL1 (required for the initiation of differentiation of leaf hair cells/ trichomes), Yeast txn & telomere length proteins.	
Myc N Term	Myc amino-terminal region. The myc family belongs to the basic helix-loop-helix leucine zipper class of transcription factors. Myc forms a heterodimer with Max, and this complex regulates cell growth through direct activation of genes involved in cell replication. c-Myc can also repress the transcription of specific genes.	HLH
NAM	The NAM (no apical meristem) family is a group of transcription factors that share a highly conserved N-terminal domain of about 150 amino acids, designated the NAC domain (NAC stands for Petunia, NAM, and Arabidopsis, ATAF1, ATAF2 and CUC2). Present in monocots and dicots. Probably have roles in the regulation of embryo and flower development. Plant specific.	
NAP_FAMILY	Nucleosome assembly protein (NAP) -- histone chaperone. May be involved in regulating gene expression as a result of histone accessibility. NAP-2 (human NAP clone) can interact with both core and linker histones and recombinant NAP-2 can transfer histones onto naked DNA templates.	Histone
P53	The p53 tumor antigen is a protein found in increased amounts in a wide variety of transformed cells. p53 is probably involved in cell cycle regulation, and may be a trans-activator that acts to negatively regulate cellular division by controlling a set of genes required for this process.	
Pax	"paired box" domain -- a 124 amino-acid conserved domain -- generally located in the N-terminal section of the proteins -- function of this conserved domain is not yet known. In some of	

	the pax proteins, there is a homeobox domain upstream of the paired box. Examples: *Drosophila* segmentation pair-rule class protein paired (prd), *Drosophila* proteins Pox-meso and Pox-neuro, the PAX proteins.	
PHD	Zinc finger-like motif. Regulate the expression of the homeotic genes through a mechanism thought to involve some aspect of chromatin structure. Speculate that the PHD-fingers are protein-protein interaction domains or that they recognize a family of related targets in the nucleus such as the nucleosomal histone tails.	Zinc Finger homeodomain
POU	'POU' (pronounced 'pow') domain -- a 70 to 75 amino-acid region found upstream of a homeobox domain in some eukaryotic transcription factors. It is thought to confer high-affinity site-specific DNA-binding and to mediate cooperative protein-protein interaction on DNA. Examples: Oct genes (bind to immunoglobulim promoter octomer region to activate genes), Neuronal development genes, & *C. elegans* development genes	Homeobox
Protamine_p2	Protamine P2 can substitute for histones in the chromatin of sperm.	
Response_reg	This domain receives the signal from the sensor partner in bacterial two-component systems. It is usually found N-terminal to a DNA binding effector domain (e.g.GLD).	GLD
Rhd	Conserved domain in a family of eukaryotic transcription factors with basic impact on oncogenesis, embryonic development and differentiation including immune response and acute phase reaction -- composed of two structural domains, the N-terminal region is similar to that found in P53, whereas the C terminal region is an immunoglobulin-like fold. Examples: NF-kappa-B, RelB, *Drosophila* Dif.	
Runt	New family of heteromeric TFs.	
Scan	The SCAN domain (named after SRE-ZBP, CTfin51, AW-1 and Number 18 cDNA) is found in several zf-c2h2 proteins. This conserved domain has been shown to be able to mediate homo- and hetero-oligomerisation.	zf-c2h2
SCR	The Arabidopsis *SCARECROW* gene regulates an assymetric cell division essential for proper radial organization of root cell layers. It was tentatively described as a transcription factor based on the presence of homopolymeric stretches of several amino acids, the presence of a basic domain similar to that of the basic-leucine zipper family of transcription factors, and the presence of leucine heptad repeats. .Two *SCARECROW* homologs, *RGA* and *GA1*, are involved in the gibberellin signal transduction pathway.	
SBPB	A new family of DNA binding proteins (putative transcriptional regulators) called squamosa promoter binding proteins or SBPs that potentially regulate floral transition. The SBPs possess a bipartite nuclear localization signal, a putative acidic activation domain and a so-called SBP-box DNA binding domain motif that does not show similarity to any known DNA binding motif .	

SET	SET (Suvar3-9, Enhancer-of-zeste, & Trithorax) domains appear to be protein-protein interaction domains. It has been demonstrated that SET domains mediate interactions with a family of proteins that display similarity with dual-specificity phosphatases (dsPTPases). Link SET-domain containing components of the epigenetic regulatory machinery with signalling pathways involved in growth and differentiation. <u>Examples:</u> ASH1 protein contains a SET domain and a PHD finger (required for stable patterns of homeotic gene expression in *Drosophila*).	PHD Zinc Finger
SNF2_N	SNF2 and "others" N-terminal domain. <u>Examples:</u> This domain is found in proteins involved in a variety of processes including transcription regulation (e.g., SNF2, STH1, brahma, MOT1) , DNA repair (e.g., ERCC6, RAD16, RAD5), DNA recombination (e.g., RAD54), & chromatin unwinding (e.g., ISWI) as well as a variety of other proteins with little functional information (e.g., lodestar, ETL1).	
SRF-TF (MADS)	56 amino-acid residues – function as dimers-- commonly homeotic proteins. <u>Examples:</u> Human serum response factor (SRF), a ubiquitous nuclear protein important for cell proliferation and differentiation; homeotic proteins involved in control of floral development; yeast arginine metabolism regulation protein I, & yeast mating type specific genes.	K-box
Stat	STAT proteins (Signal Transducers and Activators of Transcription) are a family of transcription factors that are specifically activated to regulate gene transcription when cells encounter cytokines and growth factors. STAT proteins also include an SH2 domain.	
TBP	Transcription factor TFIID (or TATA-binding protein, TBP). General factor that plays a major role in the activation of eukaryotic genes transcribed by RNA polymerase II – binds the TATA box -- C-terminal domain of about 180 residues contains two conserved repeats of a 77 amino-acid region. Generates a saddle-shaped structure that sits astride the DNA.	
t-box	About 170 to 190 amino acids, known as the T-box domain. First found in mouse T locus (Brachyury) protein, a transcription factor involved in mesoderm differentiation. Essential in tissue specification, morphogenesis and organogenesis	
Tea	A DNA-binding region of about 66 to 68 amino acids which has been found in the N-terminal section of several regulatory proteins. Examples: Mammalian enhancer factor TEF-1, *Drosophila* scalloped protein (gene sd), *Emericella nidulans* regulatory protein abaA, yeast trans-acting factor TEC1, C. elegans hypothetical protein F28B12.2.	
TEO	The founding members of this gene family are teosinte-branched1 of maize and cycloidea of Antirrhinum (snapdragon), both of which are involved in the control of plant form and structure. They have limited similarity to the	

	rice DNA binding proteins PCF1and PCF2. All share a predicted basic-helix-loop-helix domain, TCP, which has been shown to be required for DNA binding of PCF1 and PCF2.	
TFIIS	Transcription factor S-II (TFIIS). Necessary for efficient RNA polymerase II transcription elongation, past template-encoded pause sites. TFIIS shows DNA-binding activity only in the presence of RNA polymerase II. Contains four cysteines that bind a zinc ion and fold in a conformation termed a 'zinc ribbon'. Examples: also includes the eukaryotic and archebacterial RNA polymerase subunits of the 15 Kd / M family, African swine fever virus protein I243L, & Vaccinia virus RNA polymerase.	
Trihelix	Plant specific domain involved in light response -- plant specific; not in Pfam.	
Transcript_fac2	Transcription factor TFIIB repeat .	
WRKY	~50-60 aa domain. Often repeated within a WRKY protein, but it may also be present as a single copy. WRKY proteins contain several general features typical of transcription factors, like putative nuclear localization signals and transcription activation domains. Founding members are ABF1 and ABF2 proteins. May be involved in regulation of sporamin and alpha-amy genes. May also play a role in the signal transduction pathway that leads to pathogenesis-related (PR) gene activation in response to pathogens.	
ZF-B box	B-box zinc finger.	Zinc Finger
ZF-C2H2	The first zinc finger class to be characterized -- the first pair of zinc coordinating residues are cysteines, while the second pair are histidines. A number of experimental reports have demonstrated the zinc- dependent DNA or RNA binding property of some members of this class. Examples: Mammalian transcription factors Sp1-4, Xenopus transcription factor TFIIIA, & *Drosophila* Hunchback and Kruppel	Zinc Finger
Zf-C3HC4	Conserved cysteine-rich domain of 40 to 60 residues (called C3HC4 zinc-finger or 'RING' finger) that binds two atoms of zinc, and is probably involved in mediating protein-protein interactions.	Zinc Finger
ZF-C4	Conserved cysteine-rich DNA-binding region of some 65 residues. Almost always the DNA-binding domain of a nuclear hormone receptor. Receptors for steroid, thyroid, and retinoid hormones belong to a family of nuclear trans-acting transcriptional regulatory factors. These proteins regulate diverse biological processes such as pattern formation, cellular differentiation and homeostasis.	Zinc Finger
ZF-CCCH	Zinc finger	Zinc Finger
ZF-CCHC	A family of CCHC zinc fingers, mostly from retroviral gag proteins (nucleocapsid). Prototype structure is from HIV. Also contains members involved in eukaryotic gene regulation, such as *C. elegans* GLH-1. Structure is an 18-residue zinc finger.	Zinc Finger
ZF-CHC2	CHC2 zinc finger	Zinc Finger

ZF-CONSTANS	CONSTANS family zinc finger. So far only reported in plants. CONSTANS (CO) gene of *Arabidopsis* promotes flowering. Some transgenic plants containing extra copies of CO flowered earlier than wild type, suggesting that CO activity is limiting on flowering time. Double mutants were constructed containing CO and mutations affecting gibberellic acid responses, meristem identity, or phytochrome function, and their phenotypes suggested a model for the role of CO in promoting flowering.	Zinc Finger
Zf-C2HC	A DNA-binding zinc finger domain. Examples: human myelin transcription factor (Myt), C. elegans hypothetical protein F52F12.6,	
ZF-MYND	DNA-binding domain found in *Drosophila* DEAF-1 protein which binds to a 120 bp homeotic response element.	
ZN_CLUS	A cysteine-rich region that binds DNA in a zinc-dependent fashion. Found in fungal transcriptional activator proteins. It has been shown that this region forms a binuclear zinc cluster where six conserved cysteines bind two zinc cations.	
ZZ	New putative zinc finger in dystrophin and other proteins. Binds calmodulin. DNA-binding not yet shown.	
ZF-NF-X1	Cysteine-rich sequence-specific DNA-binding protein. Interacts with the conserved X-box motif of the human major histocompatibility complex class II genes via a repeated Cys-His domain and functions as a transcriptional repressor.	Zinc Finger

Table 2: Transcription factors from Arabidopsis thaliana

SEQ NUM	SEQ ID	Family/Method/E-value
1	ARABL1-06-Q1-B1-F3.f3	14-3-3(HMM:0.0091)
2	934818.f2	14-3-3(HMM:0.01)
3	905536.f1	14-3-3(HMM:1.2e-33)
4	LIB3176-108-P1-K1-G9.f3	14-3-3(HMM:1.4e-05)
5	1152_5.R1010.f2	14-3-3(HMM:1.4e-62)
6	LIB3177-002-Q1-K1-C3.f2	14-3-3(HMM:1.6e-12)
7	20_2.R1010.f1	14-3-3(HMM:1.8e-180)
8	LIB3177-044-P1-K2-G11.f1	14-3-3(HMM:1.9e-07)
9	407_1.R1010.f3	14-3-3(HMM:1.9e-167)
10	LIB3176-102-P1-K1-B7.f1	14-3-3(HMM:2.3e-07)
11	jC-atXP100C251P17T7b1.f3	14-3-3(HMM:2.3e-39)
12	291_1.R1010.f1	14-3-3(HMM:2.4e-180)
13	LIB3177-033-P1-K2-D9.f2	14-3-3(HMM:2.8e-24)
14	20_3.R1010.f1	14-3-3(HMM:2.9e-180)
15	LIB23-037-Q1-E1-B5.f3	14-3-3(HMM:2e-09)
16	148_1.R1010.f2	14-3-3(HMM:3.1e-177)
17	2747674.f1	14-3-3(HMM:3.2e-11)
18	20_1.R1010.f2	14-3-3(HMM:3.2e-181)
19	936660.f2	14-3-3(HMM:3.2e-23)
20	LIB3177-009-P1-K2-E10.f1	14-3-3(HMM:3.3e-34)
21	1353_1.R1010.f3	14-3-3(HMM:3.7e-167)
22	LIB3177-003-P1-K1-A4.f3	14-3-3(HMM:4.1)
23	LIB25-074-Q1-E1-C9.f1	14-3-3(HMM:4.1e-11)
24	906111.f1	14-3-3(HMM:4.2e-09)
25	LIB24-111-Q1-E1-H3.f3	14-3-3(HMM:4e-17)
26	LIB3176-073-P1-K1-G8.f3	14-3-3(HMM:5.3e-08)
27	LIB24-100-Q1-E1-A11.f3	14-3-3(HMM:5.3e-25)
28	148_2.R1010.f1	14-3-3(HMM:5.4e-179)
29	LIB3177-050-P1-K1-F8.f2	14-3-3(HMM:5.6e-05)
30	1152_1.R1010.f2	14-3-3(HMM:5.6e-173)
31	jC-atXP74C225E18T7038d1.f2	14-3-3(HMM:5.8e-137)
32	460364.f3	14-3-3(HMM:6e-10)
33	LIB3176-055-P1-K1-H3.f1	14-3-3(HMM:7.9e-24)
34	1152_3.R1010.f3	14-3-3(HMM:8.2e-174)
35	LIB3175-053-P1-K1-F8.f2	14-3-3(HMM:9.7e-14)
36	LIB25-027-Q1-E1-A1.f1	14-3-3(HMM:9e-32)
37	38823_1.R1010.f1	ank(HMM:0.0012)
38	LIB3234-090-P1-K1-D9.f1	ank(HMM:0.0014)
39	4513_1.R1010.f1	ank(HMM:0.035)
40	4189_1.R1010.f3	ank(HMM:0.041)
41	4986_1.R1010.f2	ank(HMM:0.068)
42	11805_1.R1010.f3	ank(HMM:1.1e-07)
43	LIB24-052-Q1-E1-B5.f1	ank(HMM:1.5)
44	jC-atXLIB327401P3c07b2.f2	ank(HMM:1.7e-10)
45	16954_1.R1010.f3	ank(HMM:1e-16)
46	1643_1.R1010.f2	ank(HMM:1e-21)
47	2066_1.R1010.f2	ank(HMM:1e-21)
48	44151_1.R1010.f1	ank(HMM:2.1e-08)
49	16163_1.R1010.f1	ank(HMM:2.2e-17)
50	33294_1.R1010.f1	ank(HMM:2.3e-08)
51	jC-atXP108C153H24T7090d1.f3	ank(HMM:2.3e-08)
52	2581661.f4	ank(HMM:2.3e-10)

53	15542_1.R1010.f1	ank(HMM:2.6e-07)
54	2748147.f3	ank(HMM:2.6e-15)
55	jC-atXP108C175O12T7093d1.f2	ank(HMM:2.6e-17)
56	32724_1.R1010.f1	ank(HMM:2.7e-08)
57	133_1.R1010.f3	"ank(HMM:2e-07),btb(HMM:9.4e-05)"
58	315446.f1	ank(HMM:2e-08)
59	1643_3.R1010.f1	ank(HMM:2e-22)
60	1643_4.R1010.f1	ank(HMM:3.1e-21)
61	4734_2.R1010.f3	ank(HMM:3.1e-43)
62	5462_1.R1010.f3	ank(HMM:3.2e-07)
63	27659_1.R1010.f3	ank(HMM:3.6e-13)
64	115473_1.R1010.f4	ank(HMM:3.6e-15)
65	1517358.f2	ank(HMM:3.6e-22)
66	1643_6.R1010.f2	ank(HMM:3.6e-22)
67	31463_1.R1010.f1	ank(HMM:4.3e-09)
68	ARABL1-05-Q1-B1-C6.f1	ank(HMM:4.4e-08)
69	LIB3168-082-P1-K1-G2.f5	ank(HMM:4.5e-11)
70	1363_1.R1010.f1	ank(HMM:4.5e-22)
71	8132_1.R1010.f1	ank(HMM:5.2e-07)
72	LIB24-116-Q1-E1-B6.f1	ank(HMM:5.4e-07)
73	32109_1.R1010.f3	ank(HMM:5.5e-16)
74	496793.f2	ank(HMM:5.6e-18)
75	LIB3176-113-P2-K1-F10.f3	ank(HMM:5.7e-15)
76	482_1.R1010.f2	ank(HMM:5.8e-31)
77	6303_1.R1010.f2	ank(HMM:5.9e-24)
78	24427_2.R1010.f2	ank(HMM:6.8e-08)
79	22643_1.R1010.f2	ank(HMM:8.2e-29)
80	27727_1.R1010.f3	ank(HMM:9.3e-16)
81	2407_1.R1010.f1	ank(HMM:9.5e-19)
82	jC-atXP108C144I3T7089d1.f2	ank(HMM:9.7e-12)
83	1643_2.R1010.f3	ank(HMM:9e-23)
84	jC-atXLIB327406P3d12b2.f1	ap2-domain(HMM:0.00019)
85	LIB22-005-Q1-E1-B7.f1	ap2-domain(HMM:0.0012)
86	LIB22-061-Q1-E2-F6.f2	ap2-domain(HMM:0.0012)
87	1217112.f2	ap2-domain(HMM:0.0013)
88	2042762.f3	ap2-domain(HMM:0.0021)
89	jC-atXP123C118L9T7046d1.f6	ap2-domain(HMM:0.0041)
90	116780_2.R1010.f3	ap2-domain(HMM:0.006)
91	2218_9.R1010.f2	ap2-domain(HMM:0.0068)
92	957825.f1	ap2-domain(HMM:0.02)
93	77399_1.R1010.f1	ap2-domain(HMM:0.021)
94	935966.f1	ap2-domain(HMM:0.023)
95	LIB3176-007-P1-K1-F5.f1	ap2-domain(HMM:0.043)
96	2048257.f2	ap2-domain(HMM:0.26)
97	1082066.f2	ap2-domain(HMM:0.51)
98	413_1.R1010.f2	"ap2-domain(HMM:1.1e-24),arf(HMM:7.5),b3(HMM:2.2e-46)"
99	414_1.R1010.f3	"ap2-domain(HMM:1.1e-28),arf(HMM:5.1),b3(HMM:1.2e-46)"
100	14576_1.R1010.f2	ap2-domain(HMM:1.1e-35)
101	389_1.R1010.f2	ap2-domain(HMM:1.2e-43)

102	470_7.R1010.f2	ap2-domain(HMM:1.3e-39)
103	9451_1.R1010.f3	ap2-domain(HMM:1.4e-37)
104	387_1.R1010.f2	ap2-domain(HMM:1.4e-39)
105	957460.f3	ap2-domain(HMM:1.5e-05)
106	74978_1.R1010.f3	ap2-domain(HMM:1.5e-37)
107	LIB23-036-Q1-E1-H8.f1	ap2-domain(HMM:1.6e-09)
108	470_2.R1010.f3	ap2-domain(HMM:1.7e-42)
109	10919_1.R1010.f5	ap2-domain(HMM:1.9e-20)
110	36240_1.R1010.f2	ap2-domain(HMM:1.9e-27)
111	9415_3.R1010.f2	ap2-domain(HMM:1.9e-36)
112	2413138.f2	ap2-domain(HMM:2.1e-38)
113	388_1.R1010.f2	ap2-domain(HMM:2.1e-39)
114	385_1.R1010.f2	ap2-domain(HMM:2.1e-41)
115	jC-atXP20C113D5T7033a1.f6	ap2-domain(HMM:2.1e-41)
116	LIB3234-100-P1-K1-B11.f5	ap2-domain(HMM:2.3e-12)
117	116780_1.R1010.f2	ap2-domain(HMM:2.3e-37)
118	11322_1.R1010.f3	ap2-domain(HMM:2.4e-19)
119	8781_1.R1010.f3	ap2-domain(HMM:2.4e-39)
120	412_1.R1010.f1	ap2-domain(HMM:2.5e-41)
121	jC-atXLIB327424P2g12b2.f1	ap2-domain(HMM:2.7e-05)
122	470_1.R1010.f3	ap2-domain(HMM:2.8e-42)
123	1364_1.R1010.f2	ap2-domain(HMM:2.8e-63)
124	PLN_g1246402.f1	ap2-domain(HMM:2.9e-39)
125	LIB3177-066-P1-K1-H7.f2	ap2-domain(HMM:2e-10)
126	LIB3234-049-P1-K1-D8.f3	ap2-domain(HMM:2e-18)
127	2762444.f3	ap2-domain(HMM:2e-39)
128	77309_1.R1010.f3	ap2-domain(HMM:3.1e-22)
129	4590_2.R1010.f1	ap2-domain(HMM:3.1e-42)
130	386_1.R1010.f2	ap2-domain(HMM:3.2e-41)
131	386_2.R1010.f1	ap2-domain(HMM:3.2e-41)
132	21598_1.R1010.f2	ap2-domain(HMM:3.4e-42)
133	8451_1.R1010.f2	ap2-domain(HMM:3.5e-33)
134	7295_1.R1010.f2	ap2-domain(HMM:3.5e-37)
135	LIB3175-035-P1-K1-G5.f5	ap2-domain(HMM:3.8e-31)
136	1913_1.R1010.f2	ap2-domain(HMM:3.8e-67)
137	15669_1.R1010.f2	ap2-domain(HMM:3.9e-14)
138	4979_1.R1010.f3	ap2-domain(HMM:3.9e-30)
139	378_1.R1010.f2	ap2-domain(HMM:4.2e-38)
140	1216985.f3	ap2-domain(HMM:4.2e-41)
141	2218_5.R1010.f2	ap2-domain(HMM:4.2e-41)
142	1158470.f3	ap2-domain(HMM:4.3e-08)
143	20544_1.R1010.f2	ap2-domain(HMM:4.6e-39)
144	jC-atXLIB327438P1e09a1.f1	ap2-domain(HMM:4.7e-35)
145	LIB3168-022-P1-K1-G5.f2	ap2-domain(HMM:4.7e-40)
146	LIB3234-018-P1-K1-F10.f3	ap2-domain(HMM:5.5)
147	30840_1.R1010.f2	ap2-domain(HMM:5.5e-37)
148	7300_1.R1010.f2	ap2-domain(HMM:5.7e-37)
149	375_1.R1010.f3	ap2-domain(HMM:5.8e-38)
150	128405_1.R1010.f4	ap2-domain(HMM:5.9)
151	PLN_g3738231.f3	ap2-domain(HMM:5e-39)
152	477_1.R1010.f1	ap2-domain(HMM:6.1e-38)
153	LIB3176-113-P2-K1-C5.f2	ap2-domain(HMM:6.2e-14)
154	9415_2.R1010.f1	ap2-domain(HMM:6.2e-27)
155	935657.f3	ap2-domain(HMM:6.3e-14)

156	5895_1.R1010.f2	ap2-domain(HMM:6.5e-30)
157	PLN_g4128207.f2	ap2-domain(HMM:6.6e-39)
158	jC-atXP100C251N4T7b1.f1	ap2-domain(HMM:6e-31)
159	75807_1.R1010.f3	ap2-domain(HMM:6e-39)
160	375_2.R1010.f2	ap2-domain(HMM:7.7e-38)
161	470_8.R1010.f3	ap2-domain(HMM:7.8e-05)
162	2597552.f3	ap2-domain(HMM:8.2e-33)
163	PLN_g541772.f2	ap2-domain(HMM:8.3e-41)
164	10231_1.R1010.f2	ap2-domain(HMM:8.7e-39)
165	375_3.R1010.f2	ap2-domain(HMM:8.8e-37)
166	138198_1.R1010.f2	ap2-domain(HMM:9.7e-35)
167	2722927.f2	ap2-domain(HMM:9.9e-05)
168	LIB24-015-Q1-E1-H9.f1	"arf(HMM:0.013),iaa(HMM:4.1)"
169	LIB3168-057-P1-K1-F8.f3	"arf(HMM:1.4e-06),b3(HMM:6e-36)"
170	1604_1.R1010.f3	"arf(HMM:1.4e-275),b3(HMM:4.1e-50),iaa(HMM:8.1e-37)"
171	2121_1.R1010.f3	"arf(HMM:1.8e-263),b3(HMM:1.1e-62)"
172	LIB24-061-Q1-E1-B8.f3	arf(HMM:2.6e-08)
173	LIB24-016-Q1-E1-F8.f1	arf(HMM:2.6e-12)
174	LIB24-061-Q1-E1-A11.f2	"arf(HMM:2.9e-13),b3(HMM:1.4e-05)"
175	LIB146-023-Q1-E1-C1.f3	arf(HMM:2.9e-27)
176	25573_1.R1010.f2	arf(HMM:2e-21)
177	1665_1.R1010.f1	"arf(HMM:3.5e-278),b3(HMM:2.5e-49),iaa(HMM:1.1e-37)"
178	1572_1.R1010.f3	"arf(HMM:3.7e-284),b3(HMM:1.7e-49),iaa(HMM:3.7e-39)"
179	LIB146-005-Q1-E1-D6.f1	arf(HMM:3.7e-38)
180	jC-atXLIB327439P2d08b2.f2	arf(HMM:5.5e-19)
181	5161_1.R1010.f3	arf(HMM:6.2e-05)
182	1652_1.R1010.f2	"arf(HMM:6.6e-277),b3(HMM:8.7e-57),iaa(HMM:7.8e-41)"
183	LIB22-009-Q1-E1-D10.f2	"arf(HMM:6.9e-11),b3(HMM:2.3e-23)"
184	1571_1.R1010.f2	"arf(HMM:7.5e-277),b3(HMM:9.9e-56),iaa(HMM:1.9e-41)"
185	2103_1.R1010.f2	"arf(HMM:9.5e-270),b3(HMM:3.2e-61),iaa(HMM:2.4e-46)"
186	25949_1.R1010.f1	arid(HMM:0.45)
187	45225_1.R1010.f1	arid(HMM:1.3e-05)
188	LIB25-100-Q1-E1-A9.f4	arid(HMM:1.5e-05)
189	2759573.f1	arid(HMM:9.5e-05)
190	jC-atXP101CE1H11T7076b1.f3	athook(HMM:0.015)
191	LIB3176-050-P1-K1-H11.f1	athook(HMM:0.018)
192	2597674.f3	athook(HMM:0.021)

193	jC-atX22079Q1E1B12a1.f1	b3(HMM:0.45)
194	PLN_g3582519.f3	b3(HMM:1.6e-69)
195	458_1.R1010.f1	b3(HMM:5.5e-74)
196	LIB3168-086-P1-K1-G10.f4	bah(HMM:0.0024)
197	31695_1.R1010.f3	bah(HMM:2.9e-21)
198	PLN_g2766712.f1	"bah(HMM:3.4e-29),chromo(HMM:0.00019)"
199	30519_1.R1010.f1	bah(HMM:4.1e-08)
200	874_1.R1010.f1	bah(HMM:5.1e-103)
201	1769_1.R1010.f2	bpf-1(HMM:0)
202	108720_1.R1010.f4	bpf-1(HMM:1.2e-09)
203	17063_1.R1010.f2	bpf-1(HMM:1.9e-27)
204	92045_1.R1010.f5	bpf-1(HMM:5.6e-31)
205	LIB25-066-Q1-E1-H6.f3	bpf-1(HMM:5e-19)
206	31960_1.R1010.f3	bromodomain(HMM:0.00075)
207	56529_1.R1010.f1	bromodomain(HMM:1.4e-12)
208	1654_1.R1010.f3	bromodomain(HMM:3.3e-32)
209	LIB3176-010-P1-K1-F5.f2	bromodomain(HMM:4.6)
210	jC-atXLIB327414P4f03b2.f2	bromodomain(HMM:4e-33)
211	65236_1.R1010.f4	bromodomain(HMM:9.1e-08)
212	LIB3234-085-Q1-K1-G6.f4	btb(HMM:0.00012)
213	48681_1.R1010.f2	btb(HMM:0.0016)
214	jC-atXP31C146F3T7d2.f3	btb(HMM:0.0022)
215	5892_2.R1010.f1	btb(HMM:0.0035)
216	jC-atXLIB327402P1f07b1.f3	btb(HMM:0.01)
217	LIB25-035-Q1-E1-B3.f1	btb(HMM:0.011)
218	LIB3177-078-P1-K1-F4.f3	btb(HMM:0.019)
219	LIB24-072-Q1-E1-G1.f3	btb(HMM:0.027)
220	11482_1.R1010.f2	btb(HMM:1.1e-05)
221	7245_1.R1010.f3	btb(HMM:2e-12)
222	29152_2.R1010.f2	btb(HMM:3.1e-19)
223	2545_1.R1010.f3	btb(HMM:3.7e-17)
224	28612_1.R1010.f1	btb(HMM:3e-08)
225	LIB3234-043-P1-K1-C12.f3	btb(HMM:4.1)
226	68549_2.R1010.f5	btb(HMM:4.2e-16)
227	5877_2.R1010.f3	btb(HMM:4.3e-10)
228	LIB25-113-Q1-E1-F12.f3	btb(HMM:4.6e-06)
229	9824_1.R1010.f2	bzip(HMM:0.00027)
230	PLN_g903687.f1	bzip(HMM:0.00076)
231	11510_1.R1010.f2	bzip(HMM:0.0011)
232	PLN_g414614.f3	bzip(HMM:0.0013)
233	742_1.R1010.f3	bzip(HMM:0.0026)
234	PLN_g304112.f1	bzip(HMM:0.0047)
235	5714_2.R1010.f2	bzip(HMM:0.013)
236	78339_1.R1010.f3	bzip(HMM:1.1e-09)
237	123173_1.R1010.f3	bzip(HMM:1.2e-08)
238	1572_2.R1010.f4	bzip(HMM:1.5e-10)
239	75128_1.R1010.f6	bzip(HMM:1.6e-05)
240	26232_1.R1010.f3	bzip(HMM:1.6e-14)
241	jC-atX25035Q1E1D03a1.f4	bzip(HMM:1.7e-05)
242	61046_1.R1010.f3	bzip(HMM:1.9e-11)
243	29897_1.R1010.f3	bzip(HMM:2.1e-13)
244	12984_1.R1010.f1	bzip(HMM:2.6e-12)
245	1054_1.R1010.f1	bzip(HMM:3.2e-05)

246	LIB3177-079-P1-K1-A10.f3	bzip(HMM:3.3e-09)
247	1476_1.R1010.f3	bzip(HMM:3.3e-15)
248	76_1.R1010.f2	bzip(HMM:3.3e-15)
249	550266.f1	bzip(HMM:3.3e-22)
250	641_1.R1010.f3	bzip(HMM:3.3e-22)
251	23422_1.R1010.f3	bzip(HMM:3.8e-14)
252	11113_1.R1010.f1	bzip(HMM:4.5e-16)
253	363_1.R1010.f3	bzip(HMM:4.9e-17)
254	1251_1.R1010.f2	bzip(HMM:4e-05)
255	2733320.f1	bzip(HMM:4e-05)
256	LIB3234-037-P1-K1-B12.f3	bzip(HMM:4e-07)
257	12984_2.R1010.f3	bzip(HMM:5.1e-12)
258	120237_1.R1010.f1	bzip(HMM:5.6e-14)
259	640_1.R1010.f1	bzip(HMM:5.6e-21)
260	639_1.R1010.f1	bzip(HMM:5.8e-24)
261	70681_1.R1010.f2	bzip(HMM:6.2e-09)
262	5890_1.R1010.f1	bzip(HMM:6e-12)
263	5714_1.R1010.f1	bzip(HMM:8.4e-12)
264	jC-atXLIB327408P4a12b1.f3	bzip(HMM:9.3e-07)
265	30010_1.R1010.f1	bzip(HMM:9.5e-06)
266	24151_1.R1010.f2	"cbfd_nfyb_hmf(HMM:0.053),histone(HMM:1e-50)"
267	24151_2.R1010.f2	"cbfd_nfyb_hmf(HMM:0.053),histone(HMM:4.1e-50)"
268	9295_1.R1010.f2	"cbfd_nfyb_hmf(HMM:0.074),histone(HMM:3.1e-47)"
269	LIB3176-111-P1-K1-D7.f1	"cbfd_nfyb_hmf(HMM:0.078),histone(HMM:4e-49)"
270	751_1.R1010.f1	cbfd_nfyb_hmf(HMM:1.2e-23)
271	750_1.R1010.f1	cbfd_nfyb_hmf(HMM:1.3e-21)
272	750_2.R1010.f2	cbfd_nfyb_hmf(HMM:1.3e-21)
273	17669_1.R1010.f2	cbfd_nfyb_hmf(HMM:1.6e-29)
274	748_1.R1010.f1	cbfd_nfyb_hmf(HMM:1e-37)
275	749_1.R1010.f3	cbfd_nfyb_hmf(HMM:4.9e-39)
276	54638_1.R1010.f3	cbfd_nfyb_hmf(HMM:5.7e-22)
277	818_1.R1010.f1	cbfd_nfyb_hmf(HMM:6.3e-30)
278	LIB3176-087-P1-K1-A8.f3	cbfd_nfyb_hmf(HMM:6e-09)
279	4774_1.R1010.f2	cbfd_nfyb_hmf(HMM:8e-23)
280	LIB22-030-Q1-E1-F4.f2	chromo(HMM:0.00065)
281	8344_1.R1010.f1	chromo(HMM:4.6e-19)
282	1537_1.R1010.f3	"csd(HMM:1.3e-21),zf-cchc(HMM:2.2e-14)"
283	38643_1.R1010.f1	csd(HMM:3.2e-19)
284	1360_1.R1010.f1	"csd(HMM:4.5e-22),zf-cchc(HMM:2.2e-14)"
285	905705.f3	csd(HMM:5.3e-21)
286	22291_1.R1010.f2	csd(HMM:6.8e-23)
287	jC-atXLIB327425P3h08b1.f3	dof(HMM:0.13)
288	LIB3175-077-P1-K1-C12.f3	dof(HMM:0.64)
289	jC-atXLIB327417P2a09b1.f3	dof(HMM:1.2e-35)
290	424_1.R1010.f2	dof(HMM:1.2e-36).f
291	16909_1.R1010.f1	dof(HMM:1.4e-33)
292	jC-atXLIB327410P4h02a1.f3	dof(HMM:1.4e-34)
293	PLN_g3386547.f1	dof(HMM:1.4e-34)

294	425_1.R1010.f3	dof(HMM:1.6e-36)
295	45689_1.R1010.f3	dof(HMM:1.9e-34)
296	4477_2.R1010.f2	dof(HMM:1.9e-35)
297	PLN_g1212758.f2	dof(HMM:2.2e-36)
298	63890_1.R1010.f2	dof(HMM:2.3e-35)
299	1800_1.R1010.f2	dof(HMM:3.2e-35)
300	43095_1.R1010.f3	dof(HMM:3.5e-32)
301	8932_1.R1010.f1	dof(HMM:3.6e-35)
302	1054280.f4	dof(HMM:4.3e-35)
303	541_2.R1010.f2	dof(HMM:4.3e-36)
304	541_4.R1010.f2	dof(HMM:4.3e-36)
305	931090.f3	dof(HMM:4.6e-32)
306	100709_1.R1010.f3	dof(HMM:4.6e-36)
307	LIB22-068-Q1-E1-C6.f1	dof(HMM:5.1)
308	21243_1.R1010.f1	dof(HMM:5.1e-11)
309	13728_1.R1010.f1	dof(HMM:6.4e-33)
310	5321_1.R1010.f3	dof(HMM:6.9e-36)
311	43095_2.R1010.f2	dof(HMM:8.2e-32)
312	2763897.f2	dof(HMM:8.8e-29)
313	LIB3234-033-P1-K1-A2.f4	dpb(HMM:0.00035)
314	397339.f3	dpb(HMM:0.024)
315	11557_3.R1010.f3	dpb(HMM:1.5e-12)
316	234_1.R1010.f2	dpb(HMM:1.9e-92)
317	52206_1.R1010.f1	dpb(HMM:2.1e-66)
318	jC-atXLIB327408P4a09b1.f3	dpb(HMM:2.7e-62)
319	2581633.f5	dpb(HMM:3.2e-41)
320	LIB3175-060-P1-K1-A12.f1	dpb(HMM:3.3e-32)
321	52206_2.R1010.f1	dpb(HMM:3.6e-18)
322	75516_1.R1010.f6	dpb(HMM:4.5e-09)
323	11557_1.R1010.f2	dpb(HMM:5.6e-79)
324	LIB3168-079-P1-K1-G7.f4	enbp(HMM:1.1e-13)
325	2445996.f2	enbp(HMM:1.9e-10)
326	958145.f2	enbp(HMM:4.6e-06)
327	5646_1.R1010.f1	gata(HMM:0.016)
328	82345_1.R1010.f6	gata(HMM:0.023)
329	1457_1.R1010.f3	gata(HMM:1.1e-14)
330	1517312.f3	gata(HMM:1.1e-14)
331	1455_1.R1010.f1	gata(HMM:1.4e-14)
332	1454_1.R1010.f3	gata(HMM:1.7e-16)
333	6981_1.R1010.f2	gata(HMM:2.2e-08)
334	8123_1.R1010.f1	gata(HMM:2.2e-15)
335	1456_1.R1010.f1	gata(HMM:3.3e-15)
336	61173_2.R1010.f1	gata(HMM:3.9e-14)
337	jC-atXP102CE2F7T7b1.f6	gld-tea(HMM:0.00099)
338	25183_1.R1010.f1	gld-tea(HMM:1.1e-30)
339	28489_1.R1010.f3	gld-tea(HMM:1.1e-36)
340	118662_1.R1010.f2	gld-tea(HMM:1.7e-16)
341	487_1.R1010.f3	"gld-tea(HMM:1e-41),response_reg(HMM:7.4e-35)"
342	27775_1.R1010.f3	gld-tea(HMM:2.1e-29)
343	PLN_g3549642.f1	"gld-tea(HMM:2.3e-24),response_reg(HMM:3.3e-18)"

344	934014.f2	gld-tea(HMM:2.3e-31)
345	18366_1.R1010.f3	gld-tea(HMM:2.3e-32)
346	22389_1.R1010.f1	gld-tea(HMM:2.4e-30)
347	2759436.f2	gld-tea(HMM:2.6)
348	634463.f2	gld-tea(HMM:2.6e-30)
349	LIB22-078-Q1-E1-G2.f3	gld-tea(HMM:3.3e-41)
350	52617_1 R1010.f1	gld-tea(HMM:5.4e-37)
351	LIB24-005-Q1-E1-F2.f2	gld-tea(HMM:5.8e-06)
352	266_1.R1010.f1	"gld-tea(HMM:6.1e-43),response_reg(HMM:5.3e-34)"
353	1401_1.R1010.f2	gld-tea(HMM:6.4e-38)
354	21599_1.R1010.f1	gld-tea(HMM:8.2e-07)
355	26342_1.R1010.f3	gld-tea(HMM:8.4e-23)
356	30703_1.R1010.f1	gld-tea(HMM:8.5e-28)
357	LIB3176-021-P1-K1-G10.f1	gld-tea(HMM:8.7e-10)
358	34019_1.R1010.f2	gld-tea(HMM:8.8e-38)
359	PLN_g3549640.f3	"gld-tea(HMM:8.8e-38),response_reg(HMM:3.8e-38)"
360	jC-atXP86CG9E617d2.f3	"gld-tea(HMM:8.9e-19),response_reg(HMM:8.4e-36)"
361	102479_1.R1010.f1	gld-tea(HMM:9.2e-17)
362	LIB3176-085-P1-K1-E8.f3	hist_deacetyl(HMM:0.00075)
363	78223_1.R1010.f4	hist_deacetyl(HMM:0.0019)
364	jC-atXP118C145L23092d2.f1	hist_deacetyl(HMM:0.012)
365	2764107.f3	hist_deacetyl(HMM:0.25)
366	17470_1.R1010.f2	hist_deacetyl(HMM:1.4e-35)
367	6666_1.R1010.f2	hist_deacetyl(HMM:1.6e-16)
368	35178_1.R1010.f3	hist_deacetyl(HMM:1.7e-11)
369	1576_1.R1010.f2	hist_deacetyl(HMM:4.5e-181)
370	LIB3234-041-P1-K1-H9.f3	hist_deacetyl(HMM:7.7e-12)
371	18274_1.R1010.f1	hist_deacetyl(HMM:8.2e-18)
372	jC-alXLIB327434P1h10a1.f5	hist_deacetyl(HMM:9.3e-16)
373	2758327.f1	histone(HMM:0.0002)
374	jC-alX24124Q1E1H01b1.f3	histone(HMM:0.00055)
375	jC-atX25021Q1E1G06a1.f5	histone(HMM:0.003)
376	LIB3176-119-P2-K1-D9.f2	histone(HMM:0.0039)
377	2733927.f2	histone(HMM:0.026)
378	LIB24-135-Q1-E1-G8.f1	histone(HMM:0.05)
379	jC-atXLIB327420P2a07a2.f4	histone(HMM:0.064)
380	2597368.f1	histone(HMM:0.084)
381	jC-atXLIB327429P4a06b2.f3	histone(HMM:0.7)
382	16709.f3	histone(HMM:0.85)
383	27124_3.R1010.f1	histone(HMM:1.1)
384	936530.f1	histone(HMM:1.1)
385	716_5.R1010.f2	histone(HMM:1.1e-46)
386	LIB25-044-Q1-E1-B10.f1	histone(HMM:1.2)
387	22083_3.R1010.f3	histone(HMM:1.2e-16)
388	LIB3175-017-P1-K1-E3.f3	histone(HMM:1.2e-24)
389	2612_1.R1010.f3	histone(HMM:1.2e-43)
390	LIB3177-019-P1-K2-B11.f2	histone(HMM:1.3e-07)
391	715_1.R1010.f1	histone(HMM:1.3e-43)

392	68_1.R1010.f3	histone(HMM:1.3e-46)
393	7751_1.R1010.f2	histone(HMM:1.3e-46)
394	716_2.R1010.f2	histone(HMM:1.4e-31)
395	8542_4.R1010.f2	histone(HMM:1.4e-34)
396	8542_2.R1010.f3	histone(HMM:1.5e-12)
397	1053603.f3	histone(HMM:1.6e-27)
398	11560_1.R1010.f3	histone(HMM:1e-18)
399	13777_1.R1010.f1	histone(HMM:1e-18)
400	13777_2.R1010.f2	histone(HMM:1e-18)
401	22083_1.R1010.f3	histone(HMM:1e-18)
402	22083_2.R1010.f1	histone(HMM:1e-18)
403	22083_4.R1010.f1	histone(HMM:1e-18)
404	LIB3176-057-P1-K1-D11.f1	histone(HMM:1e-46)
405	716_3.R1010.f3	histone(HMM:1e-48)
406	jC-atXP15C106F1T7014a1.f5	histone(HMM:1e-48)
407	10163_3.R1010.f1	histone(HMM:2.1e-29)
408	LIB24-095-Q1-E1-F3.f3	histone(HMM:2.3e-07)
409	68_6.R1010.f3	histone(HMM:2.4e-28)
410	11215_1.R1010.f3	histone(HMM:2.5e-42)
411	716_1.R1010.f2	histone(HMM:2.5e-48)
412	jC-atXLIB327420P2a03a2.f6	histone(HMM:2.8e-08)
413	LIB3176-038-P1-K1-A3.f3	histone(HMM:2.8e-40)
414	LIB3175-021-P1-K1-D3.f1	histone(HMM:3.2e-24)
415	LIB3176-027-P1-K1-F11.f2	histone(HMM:3.8e-46)
416	862_1.R1010.f1	histone(HMM:3.9e-39)
417	1217149.f2	histone(HMM:3e-27)
418	LIB3176-118-P2-K1-B11.f1	histone(HMM:3e-39)
419	LIB25-036-Q1-E1-B4.f3	histone(HMM:4.2e-14)
420	LIB25-057-Q1-E1-E3.f2	histone(HMM:4.2e-14)
421	jC-atXLIB327427P4b02a2.f5	histone(HMM:4.7e-14)
422	77_6.R1010.f1	histone(HMM:4.8e-47)
423	8542_1.R1010.f3	histone(HMM:4.8e-47)
424	8542_3.R1010.f2	histone(HMM:4.8e-47)
425	jC-atXLIB327407P1a06b2.f3	histone(HMM:4.9e-05)
426	68_5.R1010.f2	histone(HMM:4e-22)
427	LIB3175-015-P1-K1-E7.f3	histone(HMM:5.1e-15)
428	LIB25-102-Q1-E1-G8.f1	histone(HMM:5.1e-17)
429	716_6.R1010.f2	histone(HMM:5.1e-45)
430	27124_4.R1010.f3	histone(HMM:5.3e-13)
431	LIB3177-013-P1-K2-F8.f3	histone(HMM:5.3e-19)
432	8397_1.R1010.f1	histone(HMM:5.3e-52)
433	LIB25-104-Q1-E1-C11.f3	histone(HMM:5.4e-08)
434	LIB3177-019-P1-K1-B5.f2	histone(HMM:5.8)
435	10163_1.R1010.f3	histone(HMM:5.8e-50)
436	LIB24-125-Q1-E1-F5.f3	histone(HMM:6.1e-05)
437	LIB3175-033-P1-K1-A2.f1	histone(HMM:6.2e-14)
438	17255_1.R1010.f3	histone(HMM:6.5e-37)
439	jC-atXP96CH2D3T7b1.f1	histone(HMM:6.9e-44)
440	LIB3176-033-P1-K1-B1.f1	histone(HMM:7.3e-25)
441	153419_1.R1010.f3	histone(HMM:7.6e-35)
442	LIB3168-032-P1-K1-D3.f6	histone(HMM:7.8e-14)
443	13669_1.R1010.f3	histone(HMM:8.2e-07)
444	716_4.R1010.f2	histone(HMM:8.3e-26)
445	2733879.f3	histone(HMM:8.4e-11)

446	LIB3177-096-P1-K1-A8.f2	histone(HMM:8.8e-19)
447	27124_1.R1010.f3	histone(HMM:9.5e-50)
448	2758283.f1	histone(HMM:9.7e-13)
449	31420_1.R1010.f3	hlh(HMM:0.0018)
450	LIB3176-112-P1-K1-G6.f1	hlh(HMM:0.0038)
451	jC-atXB810f2.f5	hlh(HMM:0.0055)
452	17198_1.R1010.f2	hlh(HMM:0.008)
453	87116_1.R1010.f4	hlh(HMM:0.013)
454	117793_1.R1010.f1	hlh(HMM:0.019)
455	119888_1.R1010.f1	hlh(HMM:0.025)
456	71697_1.R1010.f3	hlh(HMM:0.04)
457	116704_1.R1010.f3	hlh(HMM:0.048)
458	jC-atXP104CE10B1T7b1.f3	hlh(HMM:0.08)
459	LIB24-109-Q1-E1-B3.f2	hlh(HMM:0.092)
460	35834_1.R1010.f3	hlh(HMM:0.13)
461	20469_1.R1010.f2	hlh(HMM:1.1e-07)
462	6545_1.R1010.f2	hlh(HMM:1.2e-12)
463	72703_1.R1010.f1	hlh(HMM:1.2e-14)
464	27829_1.R1010.f3	hlh(HMM:1.3e-09)
465	46829_2.R1010.f1	hlh(HMM:1.5e-07)
466	33631_1.R1010.f2	hlh(HMM:2.3e-07)
467	53493_1.R1010.f2	hlh(HMM:2.3e-12)
468	4019_2.R1010.f2	hlh(HMM:2.6e-05)
469	11026_1.R1010.f1	hlh(HMM:2.7e-13)
470	10361_1.R1010.f3	hlh(HMM:2.8e-06)
471	34071_1.R1010.f1	hlh(HMM:3.1e-09)
472	115339_1.R1010.f3	hlh(HMM:3.5e-09)
473	115339_2.R1010.f2	hlh(HMM:3.5e-09)
474	1520719.f2	hlh(HMM:3.5e-09)
475	1622_1.R1010.f1	hlh(HMM:3.5e-15)
476	38578_1.R1010.f6	hlh(HMM:3.7e-09)
477	LIB24-131-Q1-E1-G6.f1	hlh(HMM:3e-07)
478	349_1.R1010.f1	hlh(HMM:4.4e-15)
479	634586.f2	hlh(HMM:6.7e-15)
480	4766_1.R1010.f3	hlh(HMM:7.1e-06)
481	4019_3.R1010.f2	hlh(HMM:7.3e-07)
482	ARABL1-044-Q1-E1-D5.f4	hlh(HMM:7.8e-05)
483	jC-atXP123C118M3T7086a1.f4	hlh(HMM:7.9e-12)
484	LIB3234-048-P1-K1-B10.f3	hlh(HMM:7e-05)
485	1828_1.R1010.f1	hlh(HMM:8.7e-17)
486	32520_1.R1010.f1	hlh(HMM:8.8e-10)
487	jC-atXB810a2.f5	hlh(HMM:9.3)
488	501883.f5	hlh(HMM:9.7)
489	80254_1.R1010.f4	hmg_box(HMM:0.0019)
490	jC-alXLIB327436P3d04b1.f2	hmg_box(HMM:0.0021)
491	jC-atXP26C128I4T7007a1.f6	hmg_box(HMM:0.0023)
492	jC-atXP26C126I14T7089a1.f6	hmg_box(HMM:0.0031)
493	jC-atXP53C184I7T7093d1.f2	hmg_box(HMM:0.0039)
494	LIB3176-115-P2-K1-H1.f1	hmg_box(HMM:0.0078)
495	jC-atXP26C126F19T7049a1.f6	hmg_box(HMM:0.015)
496	16353_1.R1010.f1	hmg_box(HMM:0.016)
497	879_1.R1010.f3	hmg_box(HMM:1.1e-25)
498	876_10.R1010.f2	hmg_box(HMM.1.2e-17)
499	jC-atXP26C128L23T7016a1.f4	hmg_box(HMM:1.6e-09)

500	907193.f2	hmg_box(HMM:2.5e-08)
501	116866_1.R1010.f3	hmg_box(HMM:2.5e-13)
502	877_3.R1010.f2	hmg_box(HMM:2e-28)
503	876_5.R1010.f3	hmg_box(HMM:3.3e-31)
504	7619_1.R1010.f1	hmg_box(HMM:3.8e-06)
505	875_1.R1010.f2	hmg_box(HMM:3.8e-30)
506	876_1.R1010.f2	hmg_box(HMM:3.8e-31)
507	880_1.R1010.f2	hmg_box(HMM:3.9e-29)
508	jC-atXP26C124O14T7020a1.f5	hmg_box(HMM:4.2)
509	jC-atXP96CH2C4T7b1.f6	hmg_box(HMM:4.7e-23)
510	877_1.R1010.f3	hmg_box(HMM:5.2e-33)
511	877_2.R1010.f1	hmg_box(HMM:5.2e-33)
512	jC-atXP26C126K18T7090a1.f4	hmg_box(HMM:5.4e-23)
513	jC-atXP26C124N23T7004a1.f6	hmg_box(HMM:6.4e-08)
514	859_1.R1010.f3	hmg_box(HMM:8e-20)
515	903_1.R1010.f2	"homeobox(HMM:0.00014),phd(HMM:4.1e-14)"
516	1938_1.R1010.f1	"homeobox(HMM:0.00023),homeobox_knox3(5.8e-36)"
517	LIB3176-029-P1-K1-C6.f3	homeobox(HMM:0.00066)
518	515609.f1	"homeobox(HMM:0.0048),homeobox_knox3(9.0e-13),homeobox_mat(0.0006)"
519	990_1.R1010.f2	"homeobox(HMM:0.008),homeobox_knox3(7.1e-22)"
520	992_1.R1010.f2	"homeobox(HMM:0.0082),homeobox_knox3(1.7e-21)"
521	1362_1.R1010.f3	"homeobox(HMM:0.0089),homeobox_knox3(1.2e-12)"
522	991_1.R1010.f1	"homeobox(HMM:0.011),homeobox_knox3(2.4e-22)"
523	906539.f2	"homeobox(HMM:0.016),homeobox_knox3(6.5e-23)"
524	jC-atXLIB327408P2c09a1.f6	"homeobox(HMM:0.036),homeobox_knox3()3.0e-10"
525	713_1.R1010.f1	"homeobox(HMM:0.036),homeobox_knox3(4.5e-10)"
526	PLN_g424105.f3	homeobox(HMM:0.054)
527	20074_1.R1010.f2	homeobox(HMM:0.13)
528	987718.f2	homeobox(HMM:0.89)
529	24020_1.R1010.f3	homeobox(HMM:1.1e-16)
530	304_1.R1010.f1	homeobox(HMM:1.2e-17)
531	13184_1.R1010.f5	homeobox(HMM:1.2e-18)
532	906459.f3	homeobox(HMM:1.2e-18)
533	523_1.R1010.f3	homeobox(HMM:1.4e-19)
534	1945_1.R1010.f3	homeobox(HMM:1.5e-17)
535	786_1.R1010.f2	homeobox(HMM:1.6e-20)
536	jC-atXP65C208D10T7085d1.f2	homeobox(HMM:1.6e-20)
537	1548_2.R1010.f1	homeobox(HMM:1.9e-14)
538	LIB35-011-Q1-E1-H5.f3	homeobox(HMM:2.1e-08)
539	16351_1.R1010.f2	homeobox(HMM:2.3e-18)
540	PLN_g1694712.f1	homeobox(HMM:2.6e-15)
541	526_1.R1010.f3	"homeobox(HMM:2.7e-05),homeobox_knox3(1.0e-32)"

542	524_2.R1010.f2	homeobox(HMM:2.9e-11)
543	12540_1.R1010.f1	homeobox(HMM:2e-15)
544	1517240.f2	homeobox(HMM:3.4e-14)
545	787_6.R1010.f1	homeobox(HMM:3.5e-19)
546	PLN_g16333.f1	homeobox(HMM:3.5e-19)
547	PLN_g16325.f1	"homeobox(HMM:4.2e-05),phd(HMM:5.4e-14)"
548	786_5.R1010.f2	homeobox(HMM:4.2e-11)
549	9463_1.R1010.f1	homeobox(HMM:4.3e-13)
550	307_1.R1010.f1	homeobox(HMM:4.3e-15)
551	525_1.R1010.f3	homeobox(HMM:4.6e-18)
552	6707_1.R1010.f3	homeobox(HMM:4.7)
553	524_1.R1010.f3	homeobox(HMM:4.8e-19)
554	69_1.R1010.f2	homeobox(HMM:4e-16)
555	PLN_g16178.f1	homeobox(HMM:4e-16)
556	1433_1.R1010.f1	homeobox(HMM:5.1e-20)
557	306_1.R1010.f1	homeobox(HMM:5.5e-15)
558	305_1.R1010.f2	homeobox(HMM:6.4e-15)
559	63323_1.R1010.f1	homeobox(HMM:7.7e-18)
560	786_3.R1010.f1	homeobox(HMM:7.8e-16)
561	jC-atXP112C132D23T7a1.f4	homeobox(HMM:8.7e-14)
562	2759253.f6	hsf_dna-bind(HMM:0.28)
563	2996_1.R1010.f2	hsf_dna-bind(HMM:1.1e-22)
564	944_1.R1010.f1	hsf_dna-bind(HMM:1.2e-65)
565	119770_1.R1010.f1	hsf_dna-bind(HMM:1.5e-39)
566	jC-atXP124C125H21T7d1.f6	hsf_dna-bind(HMM:1.6e-11)
567	13823_1.R1010.f3	hsf_dna-bind(HMM:1e-36)
568	268_1.R1010.f1	hsf_dna-bind(HMM:2.6e-98)
569	PLN_g3256067.f1	hsf_dna-bind(HMM:3.3e-89)
570	5332_1.R1010.f3	hsf_dna-bind(HMM:6.4e-39)
571	30824_1.R1010.f2	hsf_dna-bind(HMM:8.1e-52)
572	957701.f2	hsf_dna-bind(HMM:9.9e-06)
573	32489_1.R1010.f3	hsf_dna-bind(HMM:9e-12)
574	11068_1.R1010.f2	iaa(HMM:0.0001)
575	67079_1.R1010.f5	iaa(HMM:0.00017)
576	jC-atXP66C210I12T7005a1.f4	iaa(HMM:0.0002)
577	2122_2.R1010.f2	iaa(HMM:0.00027)
578	jC-atXLIB327433P2a08a1.f6	iaa(HMM:0.00032)
579	18819_1.R1010.f1	iaa(HMM:0.00095)
580	80560_1.R1010.f4	iaa(HMM:0.0062)
581	4542_1.R1010.f3	iaa(HMM:0.034)
582	2581617.f6	iaa(HMM:0.041)
583	ARABL1-027-Q1-B1-E5.f1	iaa(HMM:0.068)
584	623623.f5	iaa(HMM:0.083)
585	1829_1.R1010.f2	iaa(HMM:1.1e-51)
586	25194_1.R1010.f2	iaa(HMM:1.2e-08)
587	183_2.R1010.f3	iaa(HMM:1.4e-54)
588	LIB3177-097-P1-K1-D6.f3	iaa(HMM:1.5e-15)
589	1980_1.R1010.f3	iaa(HMM:1.5e-69)
590	123277_1.R1010 f1	iaa(HMM:1.6e-19)
591	1827_1.R1010.f2	iaa(HMM:1 6e-68)
592	PLN_g16198.f1	iaa(HMM:1 7e-51)
593	LIB3176-041-P1-K1-A5.f3	iaa(HMM:1.9e-15)
594	2122_1.R1010.f3	iaa(HMM:1e-45)

595	jC-atXLIB327412P4c02b1.f3	iaa(HMM:1e-45)
596	45287_1.R1010.f1	iaa(HMM:1e-51)
597	jC-atXP4C88I23T7076a1.f6	iaa(HMM:2.1e-28)
598	PLN_g972932.f1	iaa(HMM:2.6e-09)
599	2581664.f6	iaa(HMM:3.1e-21)
600	78392_1.R1010.f4	iaa(HMM:3.1e-61)
601	jC-atXLIB327411P1f02a1.f5	iaa(HMM:3.4e-44)
602	183_3.R1010.f1	iaa(HMM:3.4e-58)
603	25194_2.R1010.f3	iaa(HMM:3.5e-45)
604	jC-atXP60C198O12T7040d1.f1	iaa(HMM:4.3e-12)
605	59298_1.R1010.f3	iaa(HMM:4.4e-18)
606	61018_1.R1010.f1	iaa(HMM:4.7e-07)
607	jC-atXP71C222G9T7s2.f5	iaa(HMM:6.1e-05)
608	23678_1.R1010.f2	iaa(HMM:6.9e-69)
609	210_1.R1010.f3	iaa(HMM:6e-65)
610	54_1.R1010.f2	iaa(HMM:7.1e-61)
611	jC-atXLIB327414P2b04a1.f4	iaa(HMM:7.7e-05)
612	8884_1.R1010.f3	iaa(HMM:9.3e-66)
613	LIB3177-048-P1-K1-C12.f1	iaa(HMM:9.8e-10)
614	LIB24-080-Q1-E1-D11.f1	ibr(HMM:6.6e-05)
615	906045.f2	k-box(HMM:0.0013)
616	906457.f1	"k-box(HMM:0.0081),srf-tf(HMM:2.5e-16)"
617	103229_2.R1010.f5	k-box(HMM:1.3e-23)
618	PLN_g3719214.f3	"k-box(HMM:1.3e-23),srf-tf(HMM:5.9e-34)"
619	PLN_g1737494.f1	"k-box(HMM:1.5e-32),srf-tf(HMM:1.7e-37)"
620	1917_1.R1010.f3	"k-box(HMM:1.5e-37),srf-tf(HMM:1.3e-37)"
621	jC-atX22033Q1E2A09a1.f4	k-box(HMM:1.6)
622	1583_1.R1010.f1	"k-box(HMM:1.6e-39),srf-tf(HMM:7.5e-38)"
623	508_1.R1010.f2	"k-box(HMM:1.6e-42),srf-tf(HMM:8.5e-37)"
624	738_1.R1010.f2	"k-box(HMM:1.7e-41),srf-tf(HMM:7.5e-38)"
625	740_3.R1010.f3	"k-box(HMM:1.8e-06),srf-tf(HMM:5.1e-36)"
626	PLN_g1019924.f2	"k-box(HMM:1.9e-38),srf-tf(HMM:2.9e-38)"
627	871_1.R1010.f2	"k-box(HMM:1e-28),srf-tf(HMM:1.1e-33)"
628	752_1.R1010.f2	"k-box(HMM:1e-28),srf-tf(HMM:2.4e-37)"
629	740_2.R1010.f2	"k-box(HMM:2.1e-15),srf-tf(HMM:5.1e-36)"
630	8965_1.R1010.f2	"k-box(HMM:2.2e-13),srf-tf(HMM:7.6e-36)"
631	1351_1.R1010.f3	"k-box(HMM:3.4e-41),srf-tf(HMM:2.8e-37)"
632	906325.f3	k-box(HMM:3.6e-18)
633	PLN_g862641.f2	"k-box(HMM:3.6e-32),srf-tf(HMM:1.8e-35)"

634	2747387.f1	"k-box(HMM:4.5),srf-tf(HMM:1.1e-33)"
635	1216678.f1	k-box(HMM:5.1e-15)
636	1871_1.R1010.f2	"k-box(HMM:5.2e-11),srf-tf(HMM:5.1e-32)"
637	740_1.R1010.f1	"k-box(HMM:5.6e-43),srf-tf(HMM:5.6e-36)"
638	1919_1.R1010.f1	"k-box(HMM:5e-24),srf-tf(HMM:2.6e-32)"
639	2747374.f1	"k-box(HMM:6.2),srf-tf(HMM:5e-37)"
640	504_1.R1010.f1	"k-box(HMM:6.7e-25),srf-tf(HMM:5.5e-36)"
641	119869_1.R1010.f2	k-box(HMM:6.9e-06)
642	jC-atXLIB327408P1d08b1.f3	"k-box(HMM:6.9e-15),srf-tf(HMM:8.1e-35)"
643	739_1.R1010.f2	"k-box(HMM:7.7e-40),srf-tf(HMM:1.1e-37)"
644	8965_3.R1010.f2	k-box(HMM:8.5e-13)
645	97662_1.R1010.f5	lim(HMM:0.0017)
646	1167_2.R1010.f3	lim(HMM:0.063)
647	32106_1.R1010.f2	lim(HMM:0.092)
648	13793_1.R1010.f1	lim(HMM:1.5e-33)
649	32106_2.R1010.f3	lim(HMM:1.7e-16)
650	50585_1.R1010.f2	lim(HMM:1.8e-16)
651	LIB3176-036-P1-K1-E4.f3	lim(HMM:2.2e-10)
652	1167_3.R1010.f3	lim(HMM:2.5e-15)
653	19353_2.R1010.f1	lim(HMM:3.3e-14).f
654	LIB22-059-Q1-E1-H4.f2	lim(HMM:3.4)
655	6243_1.R1010.f2	lim(HMM:4.1e-35)
656	1167_1.R1010.f2	lim(HMM:8.3e-35)
657	2763256.f1	linker_histone(HMM:0.00034)
658	LIB3176-036-P1-K1-H7.f3	linker_histone(HMM:0.00078)
659	11718_17.R1010.f1	linker_histone(HMM:0.006)
660	697_2.R1010.f2	linker_histone(HMM:0.01)
661	17727_3.R1010.f2	linker_histone(HMM:1.6e-06)
662	935999.f3	linker_histone(HMM:1.6e-28)
663	17727_2.R1010.f1	linker_histone(HMM:1.8e-10)
664	4256_1.R1010.f3	linker_histone(HMM:3.3e-22)
665	67_1.R1010.f2	linker_histone(HMM:3.3e-37)
666	127_1.R1010.f2	linker_histone(HMM:3e-22)
667	697_1.R1010.f3	linker_histone(HMM:4e-35)
668	jC-atXLIB327426P2e12b1.f1	linker_histone(HMM:5.5e-24)
669	jC-atXP79C238C1T7d2.f1	linker_histone(HMM:6.3e-15)
670	128_1.R1010.f3	linker_histone(HMM:7.8e-29)
671	128_3.R1010.f2	linker_histone(HMM:7.8e-29)
672	398632.f3	myb_dna-binding(HMM:0.00026)
673	19696_1.R1010.f3	myb_dna-binding(HMM:0.00029)
674	LIB23-041-Q1-E1-G1.f2	myb_dna-binding(HMM:0.00031)
675	51036_2.R1010.f2	myb_dna-binding(HMM:0.00038)

676	LIB3175-043-P1-K1-A3.f1	myb_dna-binding(HMM:0.00042)
677	6718 1.R1010.f1	myb_dna-binding(HMM:0.00053)
678	29160_1.R1010.f3	myb_dna-binding(HMM:0.00094)
679	LIB23-003-Q1-E1-C10.f2	myb_dna-binding(HMM:0.0012)
680	22627_1.R1010.f3	myb_dna-binding(HMM:0.0013)
681	16833.f4	myb_dna-binding(HMM:0.0015)
682	118469_1.R1010.f3	myb_dna-binding(HMM:0.0021)
683	2764125.f2	myb_dna-binding(HMM:0.0025)
684	19235_1.R1010.f3	myb_dna-binding(HMM:0.0028)
685	LIB3168-051-P1-K1-E4.f6	myb_dna-binding(HMM:0.0082)
686	116942_1.R1010.f2	myb_dna-binding(HMM:0.027)
687	LIB3175-034-P1-K1-A12.f5	myb_dna-binding(HMM:0.054)
688	59403_2.R1010.f3	myb_dna-binding(HMM:0.063)
689	70528_1.R1010.f1	myb_dna-binding(HMM:0.14)
690	LIB146-030-Q1-K1-B6.f5	myb_dna-binding(HMM:0.14)
691	906292.f2	myb_dna-binding(HMM:0.65)
692	338_2.R1010.f1	myb_dna-binding(HMM:0.85)
693	2748969.f2	myb_dna-binding(HMM:0.87)
694	PLN_g1495252.f1	myb_dna-binding(HMM:1.1e-46)
695	LIB23-037-Q1-E1-H11.f1	myb_dna-binding(HMM:1.2e-18)
696	PLN_g455462.f1	myb_dna-binding(HMM:1.2e-39)
697	PLN_g217858.f1	myb_dna-binding(HMM:1.2e-41)
698	PLN_g1254994.f1	myb_dna-binding(HMM:1.3e-41)
699	21100_1.R1010.f2	myb_dna-binding(HMM:1.3e-42)
700	337_1.R1010.f1	myb_dna-binding(HMM:1.3e-44)
701	339_1.R1010.f2	myb_dna-binding(HMM:1.3e-44)
702	LIB3168-071-P1-K1-C6.f2	myb_dna-binding(HMM:1.4e-09)
703	22848_1.R1010.f1	myb_dna-binding(HMM:1.4e-18)
704	7193_1.R1010.f2	myb_dna-binding(HMM:1.5)
705	1751_1.R1010.f2	myb_dna-binding(HMM:1.5e-37)
706	96_1.R1010.f1	myb_dna-binding(HMM:1.5e-44)
707	338_1.R1010.f3	myb_dna-binding(HMM:1.5e-45)
708	PLN_g3941471.f3	myb_dna-binding(HMM:1.6e-38)
709	125583_2.R1010.f5	myb_dna-binding(HMM:1.7)
710	jC-atXN563193a2.f2	myb_dna-binding(HMM:1.7)
711	117090_1.R1010.f1	myb_dna-binding(HMM:1.8e-17)
712	1749_1.R1010.f2	myb_dna-binding(HMM:1.8e-35)
713	33812_1.R1010.f3	myb_dna-binding(HMM:1.8e-37)
714	21524_1.R1010.f1	myb_dna-binding(HMM:1.9e-30)
715	1740_1.R1010.f1	myb_dna-binding(HMM:1.9e-40)
716	LIB22-001-Q1-E1-G3.f2	myb_dna-binding(HMM:2.1e-06)
717	10288_1.R1010.f3	myb_dna-binding(HMM:2.1e-11)
718	1748_1.R1010.f3	myb_dna-binding(HMM:2.2e-43)
719	368_1.R1010.f1	myb_dna-binding(HMM:2.2e-43)
720	25441_1.R1010.f2	myb_dna-binding(HMM:2.2e-45)
721	PLN_g1263092.f1	myb_dna-binding(HMM:2.2e-45)
722	2763242.f1	myb_dna-binding(HMM:2.3e-16)
723	PLN_g3941435.f1	myb_dna-binding(HMM:2.3e-39)
724	1753_1.R1010.f3	myb_dna-binding(HMM:2.4e-44)
725	6889_1.R1010.f3	myb_dna-binding(HMM:2.5e-09)
726	494_1.R1010.f2	myb_dna-binding(HMM:2.5e-11)

727	PLN_g1732512.f3	myb_dna-binding(HMM:2.5e-42)
728	1752_1.R1010.f2	myb_dna-binding(HMM:2.5e-45)
729	1750_1.R1010.f2	myb_dna-binding(HMM:2.6e-38)
730	1744_1.R1010.f3	myb_dna-binding(HMM:2.6e-41)
731	8478_1.R1010.f3	myb_dna-binding(HMM:2.7e-09)
732	17177_1.R1010.f3	myb_dna-binding(HMM:2.7e-31)
733	LIB3177-091-P1-K1-F4.f2	myb_dna-binding(HMM:2.9e-26)
734	LIB3177-078-P1-K1-F8.f2	myb_dna-binding(HMM:2.9e-32)
735	19235_2.R1010.f1	myb_dna-binding(HMM:2e-05)
736	367_2.R1010.f2	myb_dna-binding(HMM:3.1e-05)
737	PLN_g2280527.f1	myb_dna-binding(HMM:3.2e-42)
738	725_1.R1010.f3	myb_dna-binding(HMM:3.2e-44)
739	7193_2.R1010.f2	myb_dna-binding(HMM:3.4e-43)
740	1033_1.R1010.f1	myb_dna-binding(HMM:3.7e-41)
741	1338_1.R1010.f1	myb_dna-binding(HMM:3.8e-11)
742	LIB24-006-Q1-E1-A2.f2	myb_dna-binding(HMM:3.8e-21)
743	1023_1.R1010.f1	myb_dna-binding(HMM:4.3e-44)
744	1737_1.R1010.f1	myb_dna-binding(HMM:4.8e-47)
745	1743_1.R1010.f3	myb_dna-binding(HMM:4.9e-36)
746	PLN_g3941467.f3	myb_dna-binding(HMM:5.1e-36)
747	1333_1.R1010.f3	myb_dna-binding(HMM:5.1e-46)
748	1738_1.R1010.f3	myb_dna-binding(HMM:5.1e-46)
749	9038_1.R1010.f3	myb_dna-binding(HMM:5.3e-12)
750	1034_1.R1010.f1	myb_dna-binding(HMM:5.4e-16)
751	225_1.R1010.f3	myb_dna-binding(HMM:5.6e-42)
752	1486_1.R1010.f3	myb_dna-binding(HMM:5.8e-31)
753	936051.f1	myb_dna-binding(HMM:5.9e-14)
754	PLN_g2832407.f1	myb_dna-binding(HMM:6.1e-35)
755	1032_1.R1010.f2	myb_dna-binding(HMM:6.3e-42)
756	PLN_g2346965.f1	myb_dna-binding(HMM:6e-05)
757	LIB3175-046-P1-K1-B10.f2	myb_dna-binding(HMM:6e-22)
758	2757484.f2	myb_dna-binding(HMM:7.1e-18)
759	1772_2.R1010.f4	myb_dna-binding(HMM:7.1e-47)
760	1738_2.R1010.f3	myb_dna-binding(HMM:7.6e-34)
761	10057_1.R1010.f3	myb_dna-binding(HMM:7e-10)
762	8189_1.R1010.f3	myb_dna-binding(HMM:7e-20)
763	43001_1.R1010.f1	myb_dna-binding(HMM:8.3e-10)
764	10057_3.R1010.f3	myb_dna-binding(HMM:8.6e-10)
765	335_1.R1010.f1	myb_dna-binding(HMM:8.8e-42)
766	1747_1.R1010.f1	myb_dna-binding(HMM:8.9e-42)
767	1739_1.R1010.f1	myb_dna-binding(HMM:9.5e-44)
768	1750_2.R1010.f1	myb_dna-binding(HMM:9.6e-08)
769	LIB3175-061-P1-K1-F8.f2	nam(HMM:0.0021)
770	jC-atXLIB327424P1g06b2.f1	nam(HMM:0.0048)
771	398614.f1	nam(HMM:0.04)
772	jC-atXLIB327430P1e05b1.f1	nam(HMM:0.37)
773	LIB3175-076-P1-K1-B2.f1	nam(HMM:0.88)
774	623015.f1	nam(HMM:1.1e-05)
775	12650_4.R1010.f2	nam(HMM:1.1e-07)
776	2596320.f2	nam(HMM:1.1e-15)
777	8647_2.R1010.f2	nam(HMM:1.1e-35)
778	6414_1.R1010.f1	nam(HMM:1.1e-78)
779	LIB3234-050-P1-K1-F8.f6	nam(HMM:1.2e-09)
780	LIB3234-059-P1-K1-G11.f2	nam(HMM:1.2e-22)

781	958017.f1	nam(HMM:1.2e-26)
782	71466_1.R1010.f1	nam(HMM:1.3e-17)
783	933621.f2	nam(HMM:1.3e-26)
784	6010_1.R1010.f3	nam(HMM:1.3e-80)
785	120288_1.R1010.f1	nam(HMM:1.4e-78)
786	LIB22-002-Q1-E1-D6.f2	nam(HMM:1.5e-21)
787	LIB35-056-Q1-E2-B9.f2	nam(HMM:1.5e-47)
788	16313_1.R1010.f2	nam(HMM:1.7e-05)
789	455_1.R1010.f1	nam(HMM:1.7e-82)
790	2758682.f1	nam(HMM:1.8e-34)
791	28833_1.R1010.f3	nam(HMM:1.9e-82)
792	LIB3176-085-P1-K1-E10.f1	nam(HMM:2.1e-10)
793	LIB23-062-Q1-E1-C10.f1	nam(HMM:2.1e-23)
794	12650_1.R1010.f3	nam(HMM:2.1e-79)
795	LIB3168-082-P1-K1-A8.f1	nam(HMM:2.3e-81)
796	ARABL1-033-Q1-B1-G2.f1	nam(HMM:2.4e-58)
797	LIB23-027-Q1-E1-F3.f2	nam(HMM:2.5e-05)
798	LIB24-107-Q1-E1-D7.f2	nam(HMM:2.6e-07)
799	135_1.R1010.f1	nam(HMM:2.6e-91)
800	54574_1.R1010.f1	nam(HMM:2.7e-81)
801	LIB23-066-Q1-E1-B1.f1	nam(HMM:2.8e-33)
802	957497.f3	nam(HMM:2.8e-59)
803	23543_1.R1010.f3	nam(HMM:2e-12)
804	521_1.R1010.f3	nam(HMM:2e-85)
805	17791_1.R1010.f3	nam(HMM:3.1e-63)
806	3089_1.R1010.f2	nam(HMM:3.1e-89)
807	24699_1.R1010.f3	nam(HMM:3.4e-16)
808	19379_1.R1010.f3	nam(HMM:3.6e-50)
809	1033258.f2	nam(HMM:3e-07)
809	1033258.f2	nam(HMM:3e-07)
810	30659_1.R1010.f3	nam(HMM:4.1e-10)
811	jC-atXP123C117E1T7036d1.f6	nam(HMM:4.2e-13)
812	12539_1.R1010.f2	nam(HMM:4.4e-26)
813	2762247.f1	nam(HMM:4.5e-07)
814	jC-atXLIB327408P1d11b1.f1	nam(HMM:4.5e-59)
815	200_1.R1010.f1	nam(HMM:4.5e-90)
816	ARABL1-045-Q1-B1-E8.f1	nam(HMM:4.7e-26)
817	LIB3175-027-P1-K1-B12.f1	nam(HMM:4.9e-29)
818	76966_1.R1010.f1	nam(HMM:5.2e-09)
819	12365_1.R1010.f1	nam(HMM:5.2e-22)
820	4281_1.R1010.f3	nam(HMM:5.7e-40)
821	273_1.R1010.f3	nam(HMM:6.1e-91)
822	5370_1.R1010.f1	nam(HMM:6.2e-16)
823	LIB35-028-Q1-E1-B12.f3	nam(HMM:6.7e-06)
824	29965_1.R1010.f3	nam(HMM:6.7e-59)
825	LIB3168-083-P1-K1-F5.f2	nam(HMM:6.9e-06)
826	34649_1.R1010.f2	nam(HMM:7.3e-10)
827	12405_1.R1010.f1	nam(HMM:7.5e-10)
828	LIB24-045-Q1-E1-H6.f1	nam(HMM:7.7e-29)
829	jC-atXLIB327424P3f06b1.f3	nam(HMM:7.8)
830	33543_1.R1010.f1	nam(HMM:7e-84)
831	LIB3176-106-P1-K1-E2.f1	nam(HMM:8.3e-10)
832	LIB22-002-Q1-E1-E9.f2	nam(HMM:8.7e-11)
833	18292_1.R1010.f3	nam(HMM:8.8e-86)

834	2047367.f1	nam(HMM:9.2e-64)
834	2047367.f1	nam(HMM:9.2e-64)
835	LIB3177-007-P1-K1-E7.f2	nap_family(HMM:0.0014)
836	30951_1.R1010.f2	nap_family(HMM:0.0067)
837	906184.f1	nap_family(HMM:0.023)
838	LIB3176-036-P1-K1-A6.f1	nap_family(HMM:0.065)
839	jC-atXP62C203C3T7022a1.f6	nap_family(HMM:1.1e-05)
840	LIB3177-005-P1-K1-B6.f1	nap_family(HMM:1.4e-05)
841	LIB3175-004-P1-K1-E9.f1	nap_family(HMM:2.6e-06)
842	4462_1.R1010.f3	nap_family(HMM:3.1e-13)
843	2798_1.R1010.f2	nap_family(HMM:3e-07)
844	8405_1.R1010.f3	nap_family(HMM:4.4e-09)
845	jC-alX22045Q1E1C02b1.f1	nap_family(HMM:5.3e-15)
846	21195_1.R1010.f3	nap_family(HMM:5.6e-37)
847	LIB3177-021-P1-K2-A7.f1	nap_family(HMM:5.8e-16)
848	2852_2.R1010.f1	nap_family(HMM:7.9e-103)
849	LIB3168-067-P1-K1-F5.f2	phd(HMM:0.013)
850	1620_1.R1010.f1	phd(HMM:0.015)
851	57640_1.R1010.f2	phd(HMM:0.02)
852	1619_1.R1010.f1	phd(HMM:0.1)
853	129014_1.R1010.f3	phd(HMM:0.34)
854	LIB3234-096-P1-K1-C2.f3	phd(HMM:0.47)
855	LIB23-021-Q2-E1-C12.f3	phd(HMM:1.1e-06)
856	95652_1.R1010.f5	phd(HMM:1.5e-08)
857	LIB22-063-Q1-E1-C9.f3	phd(HMM:1.6e-12)
858	LIB3168-006-P1-K1-E7.f2	phd(HMM:2e-15)
859	jC-atXL1044Q1E1G11a1.f6	phd(HMM:3.4e-13)
860	jC-atXP60C197M21T7027a1.f4	phd(HMM:3.5e-09)
861	LIB3177-015-P1-K2-B1.f2	phd(HMM:3.7e-05)
862	157847_1.R1010.f2	phd(HMM:5.8e-09)
863	103629_1.R1010.f5	phd(HMM:7.5e-08)
864	2538_1.R1010.f2	phd(HMM:7e-12)
865	2538_3.R1010.f3	phd(HMM:7e-12)
866	jC-atXP44C171F7T7024a1.f4	phd(HMM:7e-12)
867	LIB23-031-Q1-E1-G5.f2	phd(HMM:9e-05)
868	LIB3175-033-P1-K1-E1.f1	response_reg(HMM:0.00012)
869	LIB3177-016-P1-K1-C5.f3	response_reg(HMM:0.00074)
870	LIB3177-020-P1-K1-E2.f3	response_reg(HMM:1.2)
871	LIB3176-028-P1-K1-A2.f1	response_reg(HMM:1.2e-13)
872	244_1.R1010.f1	response_reg(HMM:1.2e-23)
873	393_1.R1010.f3	response_reg(HMM:1.3e-26)
874	2413769.f2	response_reg(HMM:1.5e-06)
875	403_2.R1010.f1	response_reg(HMM:1.5e-28)
876	1327644.f3	response_reg(HMM:1.7e-09)
877	2748920.f2	response_reg(HMM:1.8e-16)
878	395_1.R1010.f1	response_reg(HMM:1.8e-27)
879	7957_1.R1010.f1	response_reg(HMM:1.8e-27)
880	21872_1.R1010.f2	response_reg(HMM:3.1e-32)
881	403_1.R1010.f1	response_reg(HMM:3.5e-29)
882	21672_1.R1010.f2	response_reg(HMM:3.8e-06)
883	PLN_g3953604.f1	response_reg(HMM:3e-10)
884	PLN_g1679802.f1	response_reg(HMM:4.1e-28)
885	256_1.R1010.f3	response_reg(HMM:4.4e-26)
886	262_1.R1010.f1	response_reg(HMM:4.4e-32)

887	PLN_g3953594.f2	response_reg(HMM:4.7e-26)
888	LIB3175-052-P1-K1-F4.f1	response_reg(HMM:5e-32)
889	jC-atXP96CH2D6T7b1.f3	response_reg(HMM:6.1e-27)
890	391_1.R1010.f1	response_reg(HMM:8.2e-27)
891	jC-atXP29C138J22T7047d1.f2	response_reg(HMM:8.8e-21)
892	8195_1.R1010.f3	sbpb(HMM:0.0021)
893	22477_2.R1010.f3	sbpb(HMM:0.0031)
894	735947.f3	sbpb(HMM:0.22)
895	22477_1.R1010.f2	sbpb(HMM:1.2e-42)
896	6824_1.R1010.f1	sbpb(HMM:4.5e-45)
897	1224_1.R1010.f1	sbpb(HMM:4.8e-46).f
898	LIB22-030-Q1-E1-F1.f2	sbpb(HMM:7.4e-46)
899	394856.f3	sbpb(HMM:8e-07)
900	1158768.f3	sbpb(HMM:9.5e-45)
901	LIB3176-024-P1-K1-G3.f1	scr(HMM:0.00023)
902	10912_3.R1010.f4	scr(HMM:0.0014)
903	LIB3168-058-P1-K1-F3.f1	scr(HMM:0.0031)
904	68978_1.R1010.f6	scr(HMM:0.01)
905	jC-atXN38694a1.f4	scr(HMM:0.03)
906	99356_1.R1010.f4	scr(HMM:1.1e-06)
907	81940_1.R1010.f5	scr(HMM:1.1e-14)
908	34737_1.R1010.f3	scr(HMM:1.2e-17)
909	115765_1.R1010.f2	scr(HMM:1.3e-05)
910	11140_1.R1010.f6	scr(HMM:1.3e-09)
911	jC-atXLIB327416P2g07a1.f6	scr(HMM:1.4e-09)
912	LIB22-025-Q1-E1-A1.f2	scr(HMM:1.4e-23)
913	139933_1.R1010.f1	scr(HMM:1.4e-31)
914	jC-atXLIB327419P1g05a2.f6	scr(HMM:1.5e-06)
915	6888_1.R1010.f3	scr(HMM:1.6e-09)
916	1156_1.R1010.f1	scr(HMM:1.7e-185)
917	222_1.R1010.f2	scr(HMM:1.8e-185)
918	LIB3177-036-P1-K1-E3.f2	scr(HMM:1.9e-05)
919	1155_2.R1010.f3	scr(HMM:1.9e-18)
920	111122_1.R1010.f4	scr(HMM:2.5e-12)
921	6443_2.R1010.f2	scr(HMM:2.8e-118)
922	5003_1.R1010.f1	scr(HMM:2e-15)
923	jC-alXLIB327434P1g12b1.f1	scr(HMM:2e-40)
924	jC-atXLIB327408P2a09a1.f6	scr(HMM:3.3e-05)
925	36525_1.R1010.f3	scr(HMM:3e-08)
926	LIB3168-028-P1-K1-B4.f6	scr(HMM:4.2e-05)
927	586965.f1	scr(HMM:4.2e-12)
928	19298_1.R1010.f1	scr(HMM:4.5e-11)
929	51773_1.R1010.f2	scr(HMM:4.6e-05)
930	LIB24-005-Q1-E1-G12.f3	scr(HMM:5.4e-09)
931	33892_1.R1010.f1	scr(HMM:5.6e-06)
932	6443_1.R1010.f1	scr(HMM:6.3e-06)
933	59776_1.R1010.f2	scr(HMM:7.1e-07)
934	39_1.R1010.f1	scr(HMM:7.4e-171)
935	87448_1.R1010.f5	scr(HMM:7.6e-15)
936	jC-atX22069Q1E1B01a1.f5	scr(HMM:7 8e-36)
937	88702_1.R1010.f1	scr(HMM:8.3e-29)
938	1155_1.R1010.f1	scr(HMM:9 2e-188)
939	LIB3177-080-P1-K1-G7.f2	set(HMM:0 0021)
940	16791.f5	set(HMM:0.0036)

941	jC-atXP32C147O24T7d2.f3	set(HMM:0.0065)
942	119988_1.R1010.f2	set(HMM:1e-23)
943	20908_1.R1010.f2	set(HMM:2.6e-45)
944	PLN_g3089624.f2	set(HMM:4.1e-55)
945	1852_1.R1010.f2	set(HMM:4.9e-56)
946	590_1.R1010.f1	set(HMM:5.4e-57)
947	5387_1.R1010.f1	set(HMM:7.1e-08)
948	LIB3234-004-P1-K1-F1.f2	set(HMM:9.1e-07)
949	1932_1.R1010.f2	snf2_n(HMM:0.1)
950	LIB22-063-Q1-E1-C6.f1	snf2_n(HMM:0.13)
951	7289_1.R1010.f1	snf2_n(HMM:0.2)
952	3933_1.R1010.f2	snf2_n(HMM:0.97)
953	117341_1.R1010.f3	snf2_n(HMM:1.1e-08)
954	1328354.f4	snf2_n(HMM:1.6e-12)
955	LIB24-048-Q1-E1-G10.f3	snf2_n(HMM:1e-16)
956	LIB24-085-Q1-E1-D12.f2	snf2_n(HMM:1e-20)
957	1328372.f3	snf2_n(HMM:2.3e-26)
958	LIB3234-006-P1-K1-H1.f1	snf2_n(HMM:3.1e-11)
959	LIB23-012-Q1-E1-G1.f2	snf2_n(HMM:3e-11)
960	LIB24-019-Q1-E1-H9.f5	snf2_n(HMM:4.9e-11)
961	28253_1.R1010.f1	srf-tf(HMM:1.1e-31)
962	5431_1.R1010.f2	srf-tf(HMM:1.1e-34)
963	jC-atXLIB327403P3h07b1.f1	srf-tf(HMM:1.4e-07)
964	LIB25-111-Q1-E1-C9.f2	srf-tf(HMM:1.5e-07)
965	LIB3177-085-P1-K1-G5.f3	srf-tf(HMM:2.9e-35)
966	14225_2.R1010.f1	srf-tf(HMM:2e-29)
967	14225_3.R1010.f2	srf-tf(HMM:2e-29)
968	30922_1.R1010.f2	srf-tf(HMM:3.3e-36)
969	jC-alX24119Q1E1A11b1.f2	srf-tf(HMM:3e-10)
970	2733904.f3	srf-tf(HMM:4.6e-23)
971	30922_2.R1010.f3	srf-tf(HMM:4.9e-07)
972	LIB24-045-Q1-E1-F2.f3	srf-tf(HMM:5.2e-05)
973	26694_1.R1010.f2	srf-tf(HMM:5.5e-18)
974	4714014.f3	srf-tf(HMM:6.1e-13)
975	LIB25-016-Q1-E1-F11.f1	srf-tf(HMM:7.5e-38)
976	26442_1.R1010.f2	srf-tf(HMM:9.8e-33)
977	jC-atXP96C249I5T7b1.f2	tbp(HMM:1.2e-38)
978	1249_2.R1010.f3	tbp(HMM:1.5e-81)
979	1249_1.R1010.f1	tbp(HMM:1.9e-80)
980	LIB3234-033-P1-K1-H1.f1	teo(HMM:0.0019)
981	jC-atXP86CG9F1T7b1.f3	teo(HMM:0.0043)
982	jC-atXP86CG9F1T7d2.f2	teo(HMM:0.006)
983	1768_1.R1010.f1	teo(HMM:1.5e-41)
984	jC-atXLIB327414P2c10a1.f3	teo(HMM:1.6e-25)
985	LIB3234-095-P1-K1-H10.f3	teo(HMM:1.9e-17)
986	14761_1.R1010.f3	teo(HMM:2.1e-36)
987	2763426.f3	teo(HMM:2.3e-16)
988	46854_1.R1010.f3	teo(HMM:2.4e-19)
989	16107_1.R1010.f3	teo(HMM:3.1e-11)
990	33449_1.R1010.f3	teo(HMM:3.1e-38)
991	27952_1.R1010.f1	teo(HMM:3.5e-36)
992	8400_2.R1010.f1	teo(HMM:4.1e-10)
993	36908_1.R1010.f1	teo(HMM:6.2e-44)
994	7511_1.R1010.f2	teo(HMM:7.3e-36)

995	7171_1.R1010.f1	teo(HMM:8.2e-33)
996	16530_1.R1010.f1	teo(HMM:9.7e-36)
997	2413898.f1	tfiis(HMM:0.015)
998	LIB23-027-Q1-E1-E11.f3	tfiis(HMM:3.6e-06)
999	1343_2.R1010.f1	transcript_fac2(HMM:0.1)
1000	35455_1.R1010.f2	transcript_fac2(HMM:0.28)
1001	1343_1.R1010.f1	transcript_fac2(HMM:3.1e-57)
1002	1271_1.R1010.f3	transcript_fac2(HMM:4.1e-59)
1003	jC-atX22014Q1E1C12a1.f6	trihelix(HMM:0.0014)
1004	103841_1.R1010.f6	trihelix(HMM:0.0024)
1005	2393630.f4	trihelix(HMM:0.0031)
1006	78762_1.R1010.f4	trihelix(HMM:0.028)
1007	jC-atXLIB327418P1a10b1.f3	trihelix(HMM:0.88)
1008	189_1.R1010.f1	trihelix(HMM:1.2e-118)
1009	LIB146-020-Q1-E1-E3.f1	trihelix(HMM:1.2e-12)
1010	852_1.R1010.f1	trihelix(HMM:1.6e-56)
1011	191_1.R1010.f1	trihelix(HMM:2.3e-120)
1012	24518_1.R1010.f2	trihelix(HMM:2.6e-07)
1013	LIB24-135-Q1-E1-H4.f1	trihelix(HMM:3.4e-53)
1014	27618_1.R1010.f1	trihelix(HMM:4.3e-07)
1015	LIB24-003-Q1-E1-D5.f3	trihelix(HMM:5.8)
1016	5312_1.R1010.f1	trihelix(HMM:6.1e-39)
1017	22425_1.R1010.f2	trihelix(HMM:7e-05)
1018	191_2.R1010.f3	trihelix(HMM:8.6e-46)
1019	jC-atXLIB327411P3d07b1.f3	wrky(HMM:0.0026)
1020	5826_1.R1010.f3	wrky(HMM:0.0031)
1021	8539_1.R1010.f1	wrky(HMM:0.0039)
1022	LIB3168-082-P1-K1-E5.f4	wrky(HMM:0.02)
1023	LIB3168-019-P1-K1-F2.f3	wrky(HMM:0.16)
1024	LIB3177-019-P1-K2-B10.f1	wrky(HMM:0.21)
1025	88718_1.R1010.f6	wrky(HMM:0.27)
1026	2393545.f2	wrky(HMM:0.34)
1027	LIB3175-020-P1-K1-G2.f1	wrky(HMM:1.1e-05)
1028	jC-atXLIB327406P2b07a1.f4	wrky(HMM:1.1e-22)
1029	1527_1.R1010.f1	wrky(HMM:1.2e-40)
1030	jC-atXP39C161C17T7s1.f2	wrky(HMM:1.4e-26)
1031	81064_1.R1010.f6	wrky(HMM:1.6e-41)
1032	9804_1.R1010.f3	wrky(HMM:1.6e-74)
1033	1327735.f2	wrky(HMM:1.7e-05)
1034	118163_1.R1010.f3	wrky(HMM:1.7e-29)
1035	LIB22-006-Q1-E1-G11.f3	wrky(HMM:1.9e-08)
1036	14802_1.R1010.f2	wrky(HMM:1.9e-35)
1037	5013_1.R1010.f2	wrky(HMM:1.9e-38)
1038	LIB22-075-Q1-E1-H8.f1	wrky(HMM:2.2e-09)
1039	jC-atXP119C193G18T7012a1.f5	wrky(HMM:2.3e-43)
1040	jC-atXP15C106F16T7018a1.f6	wrky(HMM:2.3e-45)
1041	2393223.f3	wrky(HMM:2.4e-40)
1042	15470_1.R1010.f2	wrky(HMM:2.8e-29)
1043	2759396.f3	wrky(HMM:2e-28)
1044	1479_2.R1010.f3	wrky(HMM:3.1e-86)
1045	jC-atXLIB327406P1d05b1.f2	wrky(HMM:3.2e-35)
1046	LIB3175-048-P1-K1-B6.f2	wrky(HMM:3.9e-35)
1047	56539_1.R1010.f2	wrky(HMM:4.1e-38)
1048	73241_1.R1010.f3	wrky(HMM:4.3e-24)

1049	2501_1.R1010.f1	wrky(HMM:4.4e-39)
1050	LIB3176-030-P1-K1-B12.f2	wrky(HMM:4.5e-16)
1051	773507.f4	wrky(HMM:4e-35)
1052	93888_1.R1010.f4	wrky(HMM:5.1e-42)
1053	102356_1.R1010.f6	wrky(HMM:6.6e-13)
1054	1932911.f2	wrky(HMM:7.4e-06)
1055	jC-atXP92C249D20T7085d1.f3	wrky(HMM:7.4e-07)
1056	jC-atXP15C107M17T7066a1.f4	wrky(HMM:7.8e-05)
1057	31824_1.R1010.f2	wrky(HMM:8.3e-41)
1058	9668_1.R1010.f1	"zf-b_box(HMM:0.00016),zf-constans(HMM:1.6e-33)"
1059	193_1.R1010.f2	"zf-b_box(HMM:0.0044),zf-constans(HMM:2.7e-43)"
1060	5722_1.R1010.f3	"zf-b_box(HMM:0.0063),zf-constans(HMM:8.4e-42)"
1061	LIB35-042-Q1-E1-A4.f1	"zf-b_box(HMM:0.0063),zf-constans(HMM:8.4e-42)"
1062	LIB25-027-Q1-E1-H4.f1	"zf-b_box(HMM:0.013),zf-constans(HMM:3.3e-08)"
1063	40_1.R1010.f1	"zf-b_box(HMM:0.017),zf-constans(HMM:8.1e-42)"
1064	122486_1.R1010.f3	"zf-b_box(HMM:0.028),zf-constans(HMM:5.6e-20)"
1065	PLN_g1161513.f1	"zf-b_box(HMM:0.033),zf-constans(HMM:2.1e-40)"
1066	125594_2.R1010.f2	"zf-b_box(HMM:0.039),zf-constans(HMM:3.5e-15)"
1067	51413_1.R1010.f2	"zf-b_box(HMM:0.039),zf-constans(HMM:3.6e-26)"
1068	29526_1.R1010.f3	"zf-b_box(HMM:0.042),zf-constans(HMM:7.6e-18)"
1069	1234_1.R1010.f2	"zf-b_box(HMM:0.045),zf-constans(HMM:1.7e-41)"
1070	13583_1.R1010.f2	"zf-b_box(HMM:0.053),zf-constans(HMM:3.7e-16)"
1071	17975_1.R1010.f1	"zf-b_box(HMM:0.06),zf-constans(HMM:1.1e-17)"
1072	15190_1.R1010.f2	"zf-b_box(HMM:0.063),zf-constans(HMM:2.4e-15)"
1073	jC-atXLIB327431P4f03a1.f3	"zf-b_box(HMM:0.083),zf-constans(HMM:2.9e-31)"
1074	47411_1.R1010.f2	"zf-b_box(HMM:0.096),zf-constans(HMM:2e-36)"
1075	24889_2.R1010.f3	zf-c2h2(HMM:0.00051)
1076	27999_1.R1010.f1	zf-c2h2(HMM:0.00064)
1077	jC-atXP82CG2D11T7b1.f3	zf-c2h2(HMM:0.00067)
1078	10874_2.R1010.f2	zf-c2h2(HMM:0.00069)
1079	970_1.R1010.f1	zf-c2h2(HMM:0.0013)
1080	LIB3168-010-P1-K1-G9.f3	zf-c2h2(HMM:0.0018)
1081	80711_2.R1010.f4	zf-c2h2(HMM:0.0074)
1082	jC-atXLIB327420P3h07b1.f1	zf-c2h2(HMM:0.015)
1083	PLN_g790676.f1	zf-c2h2(HMM:0.027)
1084	971_1.R1010.f2	zf-c2h2(HMM:0.064)
1085	jC-atXP5C89H13T7036a1.f6	zf-c2h2(HMM:0.064)

1086	969_1.R1010.f1	zf-c2h2(HMM:0.072)
1087	PLN_g790672.f3	zf-c2h2(HMM:0.072)
1088	PLN_g790674.f1	zf-c2h2(HMM:0.072)
1089	PLN_g1418340.f3	zf-c2h2(HMM:1.6e-07)
1090	1605_1.R1010.f1	zf-c2h2(HMM:1.9e-09)
1091	1203_1.R1010.f1	zf-c2h2(HMM:2.2e-06)
1092	5716_1.R1010.f2	zf-c2h2(HMM:2e-05)
1093	1202_1.R1010.f3	zf-c2h2(HMM:3.6e-08)
1094	PLN_g1418334.f1	zf-c2h2(HMM:3.6e-08)
1095	101520_1.R1010.f2	zf-c2h2(HMM:3.9e-09)
1096	1201_1.R1010.f1	zf-c2h2(HMM:4.5e-10)
1097	80711_1.R1010.f4	zf-c2h2(HMM:8.2e-12)
1098	1204_1.R1010.f2	zf-c2h2(HMM:8.8e-09)
1099	460754.f4	zf-c3hc4(HMM:0.00013)
1100	LIB3234-033-P1-K1-D11.f5	zf-c3hc4(HMM:0.00013)
1101	77239_1.R1010.f1	zf-c3hc4(HMM:0.00023)
1102	51315_1.R1010.f3	zf-c3hc4(HMM:0.00028)
1103	1788_1.R1010.f1	zf-c3hc4(HMM:0.00032)
1104	ARABL1-043-Q1-B1-B10.f5	zf-c3hc4(HMM:0.00038)
1105	61662_1.R1010.f1	zf-c3hc4(HMM:0.0004)
1106	65486_1.R1010.f5	zf-c3hc4(HMM:0.00054)
1107	11806_1.R1010.f1	zf-c3hc4(HMM:0.00066)
1108	2757852.f2	zf-c3hc4(HMM:0.00077)
1109	8493_1.R1010.f3	zf-c3hc4(HMM:0.00099)
1110	1520701.f1	zf-c3hc4(HMM:0.0012)
1111	jC-atX24064Q1E1E05a1.f6	zf-c3hc4(HMM:0.0015)
1112	115546_1.R1010.f6	zf-c3hc4(HMM:0.002)
1113	76250_1.R1010.f6	zf-c3hc4(HMM:0.0022)
1114	4272_5.R1010.f2	zf-c3hc4(HMM:0.0024)
1115	46964_1.R1010.f3	zf-c3hc4(HMM:0.0024)
1116	LIB3176-071-P1-K1-F4.f1	zf-c3hc4(HMM:0.0026)
1117	150482_1.R1010.f2	zf-c3hc4(HMM:0.003)
1118	jC-atXP101CE1E10T7058b1.f1	zf-c3hc4(HMM:0.003)
1119	101734_1.R1010.f1	zf-c3hc4(HMM:0.0033)
1120	jC-alXLIB327436P1g09b1.f3	zf-c3hc4(HMM:0.0054)
1121	LIB35-037-Q1-E1-D7.f2	zf-c3hc4(HMM:0.0054)
1122	13089_1.R1010.f3	zf-c3hc4(HMM:0.0064)
1123	115761_1.R1010.f1	zf-c3hc4(HMM:0.0084)
1124	458787.f4	zf-c3hc4(HMM:0.0084)
1125	88598_1.R1010.f5	zf-c3hc4(HMM:0.0099)
1126	LIB3176-086-P1-K1-F8.f1	zf-c3hc4(HMM:0.011)
1127	77842_1.R1010.f3	zf-c3hc4(HMM:0.015)
1128	88394_1.R1010.f5	zf-c3hc4(HMM:0.015)
1129	LIB25-094-Q1-E1-B8.f1	zf-c3hc4(HMM:0.015)
1130	LIB35-055-Q1-E2-H12.f2	zf-c3hc4(HMM:0.015)
1131	26804_1.R1010.f3	zf-c3hc4(HMM:0.017)
1132	44005_1.R1010.f3	zf-c3hc4(HMM:0.019)
1133	39331_1.R1010.f2	zf-c3hc4(HMM:0.023)
1134	96673_1.R1010.f4	zf-c3hc4(HMM:0.024)
1135	jC-alX24005Q1E1C11a1.f4	zf-c3hc4(HMM:0.03)
1136	634831.f1	zf-c3hc4(HMM:0.036)
1137	33548_1.R1010.f2	zf-c3hc4(HMM:0.041)
1138	33887_1.R1010.f1	zf-c3hc4(HMM:0.044)
1139	213_23.R1010.f3	zf-c3hc4(HMM:0.048)

1140	jC-atXLIB327410P2h09a1.f4	zf-c3hc4(HMM:0.049)
1141	116810_1.R1010.f3	zf-c3hc4(HMM:0.06)
1142	85162_1.R1010.f4	zf-c3hc4(HMM:0.061)
1143	88872_1.R1010.f4	zf-c3hc4(HMM:0.063)
1144	5688_2.R1010.f1	zf-c3hc4(HMM:0.065)
1145	25145_1.R1010.f6	zf-c3hc4(HMM:0.067)
1146	jC-alXLIB327434P4h12a1.f6	zf-c3hc4(HMM:0.068)
1147	LIB3177-067-P1-K1-F10.f1	zf-c3hc4(HMM:0.069)
1148	16046_1.R1010.f1	zf-c3hc4(HMM:0.072)
1149	LIB23-027-Q1-E1-H9.f6	zf-c3hc4(HMM:0.075)
1150	64121_1.R1010.f2	zf-c3hc4(HMM:0.08)
1151	91568_1.R1010.f6	zf-c3hc4(HMM:0.085)
1152	906835.f3	zf-c3hc4(HMM:0.11)
1153	75883_1.R1010.f6	zf-c3hc4(HMM:0.17)
1154	LIB35-042-Q1-E1-B5.f2	zf-c3hc4(HMM:0.22)
1155	79742_3.R1010.f4	zf-c3hc4(HMM:0.25)
1156	2749609.f3	zf-c3hc4(HMM:0.32)
1157	13387_1.R1010.f2	zf-c3hc4(HMM:0.55)
1158	36130_1.R1010.f3	zf-c3hc4(HMM:0.66)
1159	104041_1.R1010.f4	zf-c3hc4(HMM:1.1e-05)
1160	40473_1.R1010.f3	zf-c3hc4(HMM:1.1e-07)
1161	15228_1.R1010.f1	zf-c3hc4(HMM:1.1e-09)
1162	714_1.R1010.f2	"zf-c3hc4(HMM:1.1e-16),zz(HMM:4.4e-16)"
1163	jC-alXLIB327436P1g09a1.f4	zf-c3hc4(HMM:1.2e-09)
1164	2763784.f3	zf-c3hc4(HMM:1.4e-08)
1165	70486_1.R1010.f1	zf-c3hc4(HMM:1.4e-08)
1166	28736_1.R1010.f3	zf-c3hc4(HMM:1.4e-09)
1167	1793_1.R1010.f2	zf-c3hc4(HMM:1.5e-12)
1168	74196_1.R1010.f1	zf-c3hc4(HMM:1.6e-06)
1169	jC-atX24027Q1E1F03a1.f4	zf-c3hc4(HMM:1.6e-11)
1170	LIB22-004-Q1-E1-D10.f1	zf-c3hc4(HMM:1.6e-11)
1171	1785_1.R1010.f1	zf-c3hc4(HMM:1.6e-11).f
1172	2413955.f1	zf-c3hc4(HMM:1.6e-12)
1173	8878_1.R1010.f2	zf-c3hc4(HMM:1.7e-10)
1174	7144_1.R1010.f3	zf-c3hc4(HMM:1.7e-11)
1175	jC-atXP13C103O3T7004a1.f4	zf-c3hc4(HMM:1.8e-07)
1176	1786_1.R1010.f1	zf-c3hc4(HMM:1.8e-09)
1177	LIB3176-051-P1-K1-H2.f1	zf-c3hc4(HMM:1.8e-10)
1178	14579_1.R1010.f2	zf-c3hc4(HMM:1e-11)
1179	jC-atXLIB327409P4h04a1.f4	zf-c3hc4(HMM:2.1)
1180	79397_1.R1010.f5	zf-c3hc4(HMM:2.1e-11)
1181	2062852.f1	zf-c3hc4(HMM:2.2)
1182	jC-atXLIB327438P3e01a2.f2	zf-c3hc4(HMM:2.2e-09)
1183	1795_1.R1010.f2	zf-c3hc4(HMM:2.3e-09)
1184	2048291.f2	zf-c3hc4(HMM:2.3e-10)
1185	1789_1.R1010.f2	zf-c3hc4(HMM:2.4e-14)
1186	905856.f2	zf-c3hc4(HMM:2.5e-06)
1187	88949_1.R1010.f5	zf-c3hc4(HMM:2.6e-13)
1188	1787_1.R1010.f3	zf-c3hc4(HMM:2.7e-10)
1189	101518_1.R1010.f2	zf-c3hc4(HMM:2e-10)
1190	LIB23-028-Q1-E1-C3.f3	zf-c3hc4(HMM:3.1e-06)
1191	jC-atXP1C64A5T7s2.f6	zf-c3hc4(HMM:3.1e-07)
1192	74854_1.R1010.f3	zf-c3hc4(HMM:3.1e-09)

1193	ARABL1-038-Q1-E1-G10.f6	zf-c3hc4(HMM:3.1e-11)
1194	LIB3168-061-P1-K1-A9.f5	zf-c3hc4(HMM:3.2e-10)
1195	1794_1.R1010.f3	zf-c3hc4(HMM:3.3e-08)
1196	128642_1.R1010.f3	zf-c3hc4(HMM:3.4e-05)
1197	jC-atXU104f1.f4	zf-c3hc4(HMM:3.4e-05)
1198	10177_1.R1010.f1	zf-c3hc4(HMM:3.4e-06)
1199	15228_2.R1010.f3	zf-c3hc4(HMM:3.4e-10)
1200	8186_1.R1010.f3	zf-c3hc4(HMM:3.7e-06)
1201	jC-atXLIB327431P4h03a1.f2	zf-c3hc4(HMM:3.8e-07)
1202	24635_1.R1010.f3	zf-c3hc4(HMM:3.9e-08)
1203	22255_1.R1010.f1	zf-c3hc4(HMM:3.9e-09)
1204	1159615.f2	zf-c3hc4(HMM:4.2e-09)
1205	2581694.f3	zf-c3hc4(HMM:4.2e-10)
1206	jC-atXP69C219A23T7014d1.f1	zf-c3hc4(HMM:4.2e-10)
1207	17051_1.R1010.f3	zf-c3hc4(HMM:4.4e-08)
1208	1874_1.R1010.f3	zf-c3hc4(HMM:4.5e-08)
1209	1792_1.R1010.f3	zf-c3hc4(HMM:5.5e-09)
1210	6103_1.R1010.f3	zf-c3hc4(HMM:5.8e-07)
1211	14617_1.R1010.f1	zf-c3hc4(HMM:6.3e-10)
1212	2754_2.R1010.f2	zf-c3hc4(HMM:6.4e-09)
1213	101364_1.R1010.f4	zf-c3hc4(HMM:6.4e-10)
1214	jC-alXLIB327436P2d05a1.f5	zf-c3hc4(HMM:6.5e-05)
1215	24834_1.R1010.f1	zf-c3hc4(HMM:6.5e-11)
1216	4922_1.R1010.f1	zf-c3hc4(HMM:6.6e-08)
1217	15369_1.R1010.f2	zf-c3hc4(HMM:6.8e-12)
1218	949655.f1	zf-c3hc4(HMM:7.1e-07)
1219	96498_1.R1010.f6	zf-c3hc4(HMM:7.4e-08)
1220	74370_1.R1010.f2	zf-c3hc4(HMM:7.8e-06)
1221	jC-atXLIB327408P4e09a1.f4	zf-c3hc4(HMM:7.8e-10)
1222	396_1.R1010.f1	zf-c3hc4(HMM:7e-11)
1223	10338_1.R1010.f1	zf-c3hc4(HMM:8.1e-07)
1224	2047468.f3	zf-c3hc4(HMM:8.2e-05
1225	88616_1.R1010.f4	zf-c3hc4(HMM:8.6e-09)
1226	213_12.R1010.f3	zf-c3hc4(HMM:8.8e-08)
1227	2581616.f3	zf-c3hc4(HMM:8.8e-08)
1228	128926_1.R1010.f6	zf-c3hc4(HMM:8.8e-09)
1229	jC-atXP8C92K1T7d1.f4	zf-c3hc4(HMM:8.8e-12)
1230	47105_1.R1010.f2	zf-c3hc4(HMM:8e-07)
1231	57820_1.R1010.f3	zf-c3hc4(HMM:8e-12)
1232	127383_1.R1010.f4	zf-c3hc4(HMM:9.2e-13)
1233	31344_1.R1010.f3	zf-c3hc4(HMM:9.4e-06)
1234	1790_1.R1010.f2	zf-c3hc4(HMM:9.7e-12)
1235	19591_1.R1010.f3	zf-ccch(HMM:0.00014)
1236	22324_1.R1010.f2	zf-ccch(HMM:0.00034)
1237	32632_1.R1010.f1	zf-ccch(HMM:0.00038)
1238	11605_1.R1010.f3	zf-ccch(HMM:0.0018)
1239	7176_1.R1010.f3	zf-ccch(HMM:0.0023)
1240	LIB3234-087-Q1-K1-G12.f3	zf-ccch(HMM:0.0095)
1241	20290_1.R1010.f3	zf-ccch(HMM:0.0096)
1241	20290_1.R1010.f3	zf-ccch(HMM:0.0096)
1242	116042_1.R1010.f2	zf-ccch(HMM:0.015)
1243	99257_1.R1010.f6	zf-ccch(HMM:0.031)
1244	jC-atXP31C147B23T7s1.f4	zf-ccch(HMM:0.031)
1245	jC-atXLIB327416P3e02a1.f6	zf-ccch(HMM:0.04)

1246	LIB146-022-Q1-E1-E5.f2	zf-ccch(HMM:0.046)
1247	1695_1.R1010.f2	zf-ccch(HMM:0.098)
1248	116035_1.R1010.f5	zf-ccch(HMM:1.5e-05)
1249	5626_1.R1010.f3	zf-ccch(HMM:2.1e-06)
1250	8921_1.R1010.f3	zf-ccch(HMM:2.1e-06)
1251	38040_1.R1010.f1	zf-ccch(HMM:6.6e-16)
1252	1199_1.R1010.f2	zf-cchc(HMM:0.00024)
1253	670_1.R1010.f3	zf-cchc(HMM:0.0003)
1254	129921_1.R1010.f5	zf-cchc(HMM:0.00053)
1255	jC-atXLIB327433P2a10a1.f4	zf-cchc(HMM:0.0017)
1256	108675_1.R1010.f5	zf-cchc(HMM:0.012)
1257	LIB3177-077-P1-K1-E7.f1	zf-cchc(HMM:0.15)
1258	1200_1.R1010.f2	zf-cchc(HMM:1.2e-05)
1259	22484_1.R1010.f1	zf-cchc(HMM:1.5e-06)
1260	11483_1.R1010.f1	zf-cchc(HMM:1.5e-17)
1261	LIB3176-047-P1-K1-D4.f2	zf-cchc(HMM:1.7e-12)
1262	2763645.f3	zf-cchc(HMM:2.6e-06)
1263	13021_1.R1010.f3	zf-cchc(HMM:2.9e-11)
1264	3418_1.R1010.f3	zf-cchc(HMM:4.5e-05)
1265	LIB3176-069-P1-K1-H8.f2	zf-constans(HMM:0.00032)
1266	47549_1.R1010.f1	zf-constans(HMM:1.3e-14)
1267	28795_1.R1010.f2	zf-constans(HMM:1.8e-31)
1268	74055_1.R1010.f1	zf-constans(HMM:1.9e-16)
1269	315827.f3	zf-constans(HMM:1e-10)
1270	28040_1.R1010.f1	zf-constans(HMM:1e-25)
1271	131318_1.R1010.f2	zf-constans(HMM:2.1e-18)
1272	7711_1.R1010.f3	zf-constans(HMM:2.3e-14)
1273	2733155.f3	zf-constans(HMM:2.7e-12)
1274	13864_8.R1010.f1	zf-constans(HMM:3.3e-10)
1275	13864_3.R1010.f2	zf-constans(HMM:3.9e-31)
1276	906416.f3	zf-constans(HMM:4.8e-38)
1277	35325_1.R1010.f3	zf-constans(HMM:5.6e-36)
1278	1216676.f1	zf-constans(HMM:5e-07)
1279	jC-atXN442143a1.f6	zf-constans(HMM:9.6e-10)
1280	2048672.f1	zf-mynd(HMM:0.037)
1281	123095_1.R1010.f2	zf-mynd(HMM:0.27)
1282	117076_1.R1010.f6	zf-mynd(HMM:0.85)
1283	102319_2.R1010.f6	zf-mynd(HMM:2.3e-11)
1284	93572_1.R1010.f5	zz(HMM:0.045)
1285	2470_1.R1010.f1	zz(HMM:5.8e-08)
1286	550153.f2	zz(HMM:7.6e-07)

Table 3: Nucleic Acids encoding transcription factors from Arabidopsis thaliana

SEQ NUM	SEQ ID	Family/Method/E-value
1287	LIB22-064-Q1-E1-D9	14-3-3(HMM:0.00044)
1288	ARABL1-06-Q1-B1-F3	14-3-3(HMM:0.0091)
1289	934818	14-3-3(HMM:0.01)
1290	905536	14-3-3(HMM:1.2e-33)
1291	LIB3176-108-P1-K1-G9	14-3-3(HMM:1.4e-05)
1292	1152_4.R1010	14-3-3(HMM:1.4e-56)
1293	1152_5.R1010	14-3-3(HMM:1.4e-62)
1294	1152_2.R1010	14-3-3(HMM:1.5e-09)
1295	jC-atXLIB327419P4d06b1	14-3-3(HMM:1.5e-58)
1296	LIB3177-002-Q1-K1-C3	14-3-3(HMM:1.6e-12)
1297	20_2.R1010	14-3-3(HMM:1.8e-180)
1298	LIB3177-044-P1-K2-G11	14-3-3(HMM:1.9e-07)
1299	407_1.R1010	14-3-3(HMM:1.9e-167)
1300	LIB3176-102-P1-K1-B7	14-3-3(HMM:2.3e-07)
1301	jC-atXP100C251P17T7b1	14-3-3(HMM:2.3e-39)
1302	291_1.R1010	14-3-3(HMM:2.4e-180)
1303	LIB3177-033-P1-K2-D9	14-3-3(HMM:2.8e-24)
1304	20_3.R1010	14-3-3(HMM:2.9e-180)
1305	LIB23-037-Q1-E1-B5	14-3-3(HMM:2e-09)
1306	148_1.R1010	14-3-3(HMM:3.1e-177)
1307	2747674	14-3-3(HMM:3.2e-11)
1308	20_1.R1010	14-3-3(HMM:3.2e-181)
1309	936660	14-3-3(HMM:3.2e-23)
1310	LIB3177-009-P1-K2-E10	14-3-3(HMM:3.3e-34)
1311	1353_1.R1010	14-3-3(HMM:3.7e-167)
1312	2413851	14-3-3(HMM:3e-09)
1313	LIB3177-003-P1-K1-A4	14-3-3(HMM:4.1)
1314	LIB25-074-Q1-E1-C9	14-3-3(HMM:4.1e-11)
1315	906111	14-3-3(HMM:4.2e-09)
1316	20_4.R1010	14-3-3(HMM:4.6e-35)
1317	LIB24-111-Q1-E1-H3	14-3-3(HMM:4e-17)
1318	LIB3176-073-P1-K1-G8	14-3-3(HMM:5.3e-08)
1319	LIB24-100-Q1-E1-A11	14-3-3(HMM:5.3e-25)
1320	148_2.R1010	14-3-3(HMM:5.4e-179)
1321	LIB3177-050-P1-K1-F8	14-3-3(HMM:5.6e-05)
1322	1152_1.R1010	14-3-3(HMM:5.6e-173)
1323	jC-atXP74C225E18T7038d1	14-3-3(HMM:5.8e-137)
1324	460364	14-3-3(HMM:6e-10)
1325	LIB3176-055-P1-K1-H3	14-3-3(HMM:7.9e-24)
1326	1152_3.R1010	14-3-3(HMM:8.2e-174)
1327	LIB3175-053-P1-K1-F8	14-3-3(HMM:9.7e-14)
1328	LIB25-027-Q1-E1-A1	14-3-3(HMM:9e-32)
1329	38823_1.R1010	ank(HMM:0.0012)
1330	LIB3234-090-P1-K1-D9	ank(HMM:0.0014)
1331	LIB3175-052-P1-K1-H2	ank(HMM:0.005)
1332	LIB22-005-Q1-E1-C10	ank(HMM:0.018)
1333	4513_1.R1010	ank(HMM:0.035)
1334	4189_1.R1010	ank(HMM:0.041)
1335	4986_1.R1010	ank(HMM:0.068)
1336	LIB24-006-Q1-E1-B11	ank(HMM:0.14)
1337	11805_1.R1010	ank(HMM:1.1e-07)
1338	906580	ank(HMM:1.2e-05)

1339	LIB24-052-Q1-E1-B5	ank(HMM:1.5)
1340	2407_2.R1010	ank(HMM:1.7e-05)
1341	jC-atXLIB327401P3c07b2	ank(HMM:1.7e-10)
1342	16954_1.R1010	ank(HMM:1e-16)
1343	1643_1.R1010	ank(HMM:1e-21)
1344	2066_1.R1010	ank(HMM:1e-21)
1345	44151_1.R1010	ank(HMM:2.1e-08)
1346	16163_1.R1010	ank(HMM:2.2e-17)
1347	33294_1.R1010	ank(HMM:2.3e-08)
1348	jC-atXP108C153H24T7090d1	ank(HMM:2.3e-08)
1349	2581661	ank(HMM:2.3e-10)
1350	15542_1.R1010	ank(HMM:2.6e-07)
1351	2748147	ank(HMM:2.6e-15)
1352	jC-atXP108C175O12T7093d1	ank(HMM:2.6e-17)
1353	32724_1.R1010	ank(HMM:2.7e-08)
1354	133_1.R1010	"ank(HMM:2e-07),btb(HMM:9.4e-05)"
1355	315446	ank(HMM:2e-08)
1356	1643_3.R1010	ank(HMM:2e-22)
1357	1643_4.R1010	ank(HMM:3.1e-21)
1358	4734_2.R1010	ank(HMM:3.1e-43)
1359	5462_1.R1010	ank(HMM:3.2e-07)
1360	27659_1.R1010	ank(HMM:3.6e-13)
1361	115473_1.R1010	ank(HMM:3.6e-15)
1362	1517358	ank(HMM:3.6e-22)
1363	1643_6.R1010	ank(HMM:3.6e-22)
1364	4821_1.R1010	ank(HMM:4.1e-07)
1365	31463_1.R1010	ank(HMM:4.3e-09)
1366	ARABL1-05-Q1-B1-C6	ank(HMM:4.4e-08)
1367	LIB3168-082-P1-K1-G2	ank(HMM:4.5e-11)
1368	1363_1.R1010	ank(HMM:4.5e-22)
1369	8132_1.R1010	ank(HMM:5.2e-07)
1370	LIB24-116-Q1-E1-B6	ank(HMM:5.4e-07)
1371	32109_1.R1010	ank(HMM:5.5e-16)
1372	496793	ank(HMM:5.6e-18)
1373	LIB3176-113-P2-K1-F10	ank(HMM:5.7e-15)
1374	482_1.R1010	ank(HMM:5.8e-31)
1375	6303_1.R1010	ank(HMM:5.9e-24)
1376	24427_2.R1010	ank(HMM:6.8e-08)
1377	22643_1.R1010	ank(HMM:8.2e-29)
1378	27727_1.R1010	ank(HMM:9.3e-16)
1379	2407_1.R1010	ank(HMM:9.5e-19)
1380	jC-atXP108C144I3T7089d1	ank(HMM:9.7e-12)
1381	1643_2.R1010	ank(HMM:9e-23)
1382	jC-atXLIB327406P3d12b2	ap2-domain(HMM:0.00019)
1383	LIB22-005-Q1-E1-B7	ap2-domain(HMM:0.0012)
1384	LIB22-061-Q1-E2-F6	ap2-domain(HMM:0.0012)
1385	1217112	ap2-domain(HMM:0.0013)
1386	2042762	ap2-domain(HMM:0.0021)
1387	jC-atXP123C118L9T7046d1	ap2-domain(HMM:0.0041)
1388	116780_2.R1010	ap2-domain(HMM:0.006)
1389	2218_9.R1010	ap2-domain(HMM:0.0068)
1390	957825	ap2-domain(HMM:0.02)
1391	77399_1.R1010	ap2-domain(HMM:0.021)

1392	935966	ap2-domain(HMM:0.023)
1393	LIB3176-007-P1-K1-F5	ap2-domain(HMM:0.043)
1394	2048257	ap2-domain(HMM:0.26)
1395	1082066	ap2-domain(HMM:0.51)
1396	413_1.R1010	"ap2-domain(HMM:1.1e-24),arf(HMM:7.5),b3(HMM:2.2e-46)"
1397	414 1.R1010	"ap2-domain(HMM:1.1e-28),arf(HMM:5.1),b3(HMM:1.2e-46)"
1398	14576_1.R1010	ap2-domain(HMM:1.1e-35)
1399	389_1.R1010	ap2-domain(HMM:1.2e-43)
1400	470_7.R1010	ap2-domain(HMM:1.3e-39)
1401	9451_1.R1010	ap2-domain(HMM:1.4e-37)
1402	387_1.R1010	ap2-domain(HMM:1.4e-39)
1403	957460	ap2-domain(HMM:1.5e-05)
1404	74978_1.R1010	ap2-domain(HMM:1.5e-37)
1405	LIB23-036-Q1-E1-H8	ap2-domain(HMM:1.6e-09)
1406	470_2.R1010	ap2-domain(HMM:1.7e-42)
1407	10919_1.R1010	ap2-domain(HMM:1.9e-20)
1408	36240_1.R1010	ap2-domain(HMM:1.9e-27)
1409	9415_3.R1010	ap2-domain(HMM:1.9e-36)
1410	2413138	ap2-domain(HMM:2.1e-38)
1411	388_1.R1010	ap2-domain(HMM:2.1e-39)
1412	385_1.R1010	ap2-domain(HMM:2.1e-41)
1413	jC-atXP20C113D5T7033a1	ap2-domain(HMM:2.1e-41)
1414	LIB3234-100-P1-K1-B11	ap2-domain(HMM:2.3e-12)
1415	116780_1.R1010	ap2-domain(HMM:2.3e-37)
1416	11322_1.R1010	ap2-domain(HMM:2.4e-19)
1417	8781_1.R1010	ap2-domain(HMM:2.4e-39)
1418	412_1.R1010	ap2-domain(HMM:2.5e-41)
1419	jC-atXLIB327424P2g12b2	ap2-domain(HMM:2.7e-05)
1420	470_1.R1010	ap2-domain(HMM:2.8e-42)
1421	1364_1.R1010	ap2-domain(HMM:2.8e-63)
1422	PLN_g1246402	ap2-domain(HMM:2.9e-39)
1423	LIB3177-066-P1-K1-H7	ap2-domain(HMM:2e-10)
1424	LIB3234-049-P1-K1-D8	ap2-domain(HMM:2e-18)
1425	2762444	ap2-domain(HMM:2e-39)
1426	9415_1.R1010	ap2-domain(HMM:3.1)
1427	77309_1.R1010	ap2-domain(HMM:3.1e-22)
1428	4590_2.R1010	ap2-domain(HMM:3.1e-42)
1429	386_1.R1010	ap2-domain(HMM:3.2e-41)
1430	386_2.R1010	ap2-domain(HMM:3.2e-41)
1431	21598_1.R1010	ap2-domain(HMM:3.4e-42)
1432	8451_1.R1010	ap2-domain(HMM:3.5e-33)
1433	7295_1.R1010	ap2-domain(HMM:3.5e-37)
1434	LIB3175-035-P1-K1-G5	ap2-domain(HMM:3.8e-31)
1435	1913_1.R1010	ap2-domain(HMM:3.8e-67)
1436	19728_1.R1010	ap2-domain(HMM:3.9e-07)
1437	15669_1.R1010	ap2-domain(HMM:3.9e-14)
1438	4979_1.R1010	ap2-domain(HMM:3.9e-30)
1439	378_1.R1010	ap2-domain(HMM:4.2e-38)
1440	1216985	ap2-domain(HMM:4.2e-41)
1441	2218_5.R1010	ap2-domain(HMM:4.2e-41)

1442	1158470	ap2-domain(HMM:4.3e-08)
1443	20544_1.R1010	ap2-domain(HMM:4.6e-39)
1444	jC-atXLIB327438P1e09a1	ap2-domain(HMM:4.7e-35)
1445	LIB3168-022-P1-K1-G5	ap2-domain(HMM:4.7e-40)
1446	LIB3234-018-P1-K1-F10	ap2-domain(HMM:5.5)
1447	30840_1.R1010	ap2-domain(HMM:5.5e-37)
1448	7300_1.R1010	ap2-domain(HMM:5.7e-37)
1449	375_1.R1010	ap2-domain(HMM:5.8e-38)
1450	128405_1.R1010	ap2-domain(HMM:5.9)
1451	PLN_g3738231	ap2-domain(HMM:5e-39)
1452	477_1.R1010	ap2-domain(HMM:6.1e-38)
1453	LIB3176-113-P2-K1-C5	ap2-domain(HMM:6.2e-14)
1454	9415_2.R1010	ap2-domain(HMM:6.2e-27)
1455	935657	ap2-domain(HMM:6.3e-14)
1456	5895_1.R1010	ap2-domain(HMM:6.5e-30)
1457	PLN_g4128207	ap2-domain(HMM:6.6e-39)
1458	jC-atXP100C251N4T7b1	ap2-domain(HMM:6e-31)
1459	75807_1.R1010	ap2-domain(HMM:6e-39)
1460	375_2.R1010	ap2-domain(HMM:7.7e-38)
1461	470_8.R1010	ap2-domain(HMM:7.8e-05)
1462	2597552	ap2-domain(HMM:8.2e-33)
1463	PLN_g541772	ap2-domain(HMM:8.3e-41)
1464	10231_1.R1010	ap2-domain(HMM:8.7e-39)
1465	375_3.R1010	ap2-domain(HMM:8.8e-37)
1466	138198_1.R1010	ap2-domain(HMM:9.7e-35)
1467	2722927	ap2-domain(HMM.9.9e-05)
1468	LIB24-015-Q1-E1-H9	"arf(HMM:0.013),iaa(HMM:4.1)"
1469	LIB3168-057-P1-K1-F8	"arf(HMM:1.4e-06),b3(HMM:6e-36)"
1470	1604_1.R1010	"arf(HMM:1.4e-275),b3(HMM:4.1e-50),iaa(HMM:8.1e-37)"
1471	2121_1.R1010	"arf(HMM:1.8e-263),b3(HMM:1.1e-62)"
1472	LIB24-061-Q1-E1-B8	arf(HMM:2.6e-08)
1473	LIB24-016-Q1-E1-F8	arf(HMM:2.6e-12)
1474	LIB24-061-Q1-E1-A11	"arf(HMM:2.9e-13),b3(HMM:1.4e-05)"
1475	LIB146-023-Q1-E1-C1	arf(HMM:2.9e-27)
1476	25573_1.R1010	arf(HMM:2e-21)
1477	jC-atXLIB327404P1b06b1	"arf(HMM:3.4e-22),b3(HMM:3.1e-11)"
1478	1665_1.R1010	"arf(HMM:3.5e-278),b3(HMM:2.5e-49),iaa(HMM:1.1e-37)"
1479	1572_1.R1010	"arf(HMM:3.7e-284),b3(HMM:1.7e-49),iaa(HMM:3.7e-39)"
1480	LIB146-005-Q1-E1-D6	arf(HMM:3.7e-38)
1481	jC-atXLIB327439P2d08b2	arf(HMM:5.5e-19)
1482	5161_1.R1010	arf(HMM:6.2e-05)
1483	1652_1.R1010	"arf(HMM:6.6e-277),b3(HMM:8.7e-

		57),iaa(HMM:7.8e-41)"
1484	LIB22-009-Q1-E1-D10	"arf(HMM:6.9e-11),b3(HMM:2.3e-23)"
1485	1571_1.R1010	"arf(HMM:7.5e-277),b3(HMM:9.9e-56),iaa(HMM:1.9e-41)"
1486	2103_1.R1010	"arf(HMM:9.5e-270),b3(HMM:3.2e-61),iaa(HMM:2.4e-46)"
1487	25949_1.R1010	arid(HMM:0.45)
1488	45225_1.R1010	arid(HMM:1.3e-05)
1489	LIB25-100-Q1-E1-A9	arid(HMM:1.5e-05)
1490	2759573	arid(HMM:9.5e-05)
1491	jC-atXP101CE1H11T7076b1	athook(HMM:0.015)
1492	LIB3176-050-P1-K1-H11	athook(HMM:0.018)
1493	2597674	athook(HMM:0.021)
1494	jC-atX22079Q1E1B12a1	b3(HMM:0.45)
1495	PLN_g3582519	b3(HMM:1.6e-69)
1496	458_1.R1010	b3(HMM:5.5e-74)
1497	LIB3168-086-P1-K1-G10	bah(HMM:0.0024)
1498	31695_1.R1010	bah(HMM:2.9e-21)
1499	PLN_g2766712	"bah(HMM:3.4e-29),chromo(HMM:0.00019)"
1500	30519_1.R1010	bah(HMM:4.1e-08)
1501	874_1.R1010	bah(HMM:5.1e-103)
1502	1769_1.R1010	bpf-1(HMM:0)
1503	11707_1.R1010	bpf-1(HMM:0.047)
1504	108720_1.R1010	bpf-1(HMM:1.2e-09)
1505	LIB3176-033-P1-K1-D4	bpf-1(HMM:1.4e-20)
1506	17063_1.R1010	bpf-1(HMM:1.9e-27)
1507	40300_1.R1010	bpf-1(HMM:4.9e-58)
1508	92045_1.R1010	bpf-1(HMM:5.6e-31)
1509	LIB25-066-Q1-E1-H6	bpf-1(HMM:5e-19)
1510	31960_1.R1010	bromodomain(HMM:0.00075)
1511	56529_1.R1010	bromodomain(HMM:1.4e-12)
1512	1654_1.R1010	bromodomain(HMM:3.3e-32)
1513	LIB3176-010-P1-K1-F5	bromodomain(HMM:4.6)
1514	jC-atXLIB327414P4f03b2	bromodomain(HMM:4e-33)
1515	65236_1.R1010	bromodomain(HMM:9.1e-08)
1516	LIB3234-085-Q1-K1-G6	btb(HMM:0.00012)
1517	48681_1.R1010	btb(HMM:0.0016)
1518	jC-atXP31C146F3T7d2	btb(HMM:0.0022)
1519	5892_2.R1010	btb(HMM:0.0035)
1520	jC-atXLIB327402P1f07b1	btb(HMM:0.01)
1521	LIB25-035-Q1-E1-B3	btb(HMM:0.011)
1522	LIB3177-078-P1-K1-F4	btb(HMM:0.019)
1523	LIB24-072-Q1-E1-G1	btb(HMM:0.027)
1524	11482_1.R1010	btb(HMM:1.1e-05)
1525	3918_1.R1010	btb(HMM:1.6e-05)
1526	7245_1.R1010	btb(HMM:2e-12)
1527	29152_2.R1010	btb(HMM:3.1e-19)
1528	2545_1.R1010	btb(HMM:3.7e-17)
1529	28612_1.R1010	btb(HMM:3e-08)
1530	LIB3234-043-P1-K1-C12	btb(HMM:4.1)

1531	68549_2.R1010	btb(HMM:4.2e-16)
1532	5877_2.R1010	btb(HMM:4.3e-10)
1533	LIB25-113-Q1-E1-F12	btb(HMM:4.6e-06)
1534	9824_1.R1010	bzip(HMM:0.00027)
1535	PLN_g903687	bzip(HMM:0.00076)
1536	11510_1.R1010	bzip(HMM:0.0011)
1537	PLN_g414614	bzip(HMM:0.0013)
1538	742_1.R1010	bzip(HMM:0.0026)
1539	PLN_g304112	bzip(HMM:0.0047)
1540	5714_2.R1010	bzip(HMM:0.013)
1541	78339_1.R1010	bzip(HMM:1.1e-09)
1542	123173_1.R1010	bzip(HMM:1.2e-08)
1543	1572_2.R1010	bzip(HMM:1.5e-10)
1544	75128_1.R1010	bzip(HMM:1.6e-05)
1545	26232_1.R1010	bzip(HMM:1.6e-14)
1546	jC-atX25035Q1E1D03a1	bzip(HMM:1.7e-05)
1547	61046_1.R1010	bzip(HMM:1.9e-11)
1548	29897_1.R1010	bzip(HMM:2.1e-13)
1549	12984_1.R1010	bzip(HMM:2.6e-12)
1550	1054_1.R1010	bzip(HMM:3.2e-05)
1551	LIB3177-079-P1-K1-A10	bzip(HMM:3.3e-09)
1552	1476_1.R1010	bzip(HMM:3.3e-15)
1553	76_1.R1010	bzip(HMM:3.3e-15)
1554	550266	bzip(HMM:3.3e-22)
1555	641_1.R1010	bzip(HMM:3.3e-22)
1556	23422_1.R1010	bzip(HMM:3.8e-14)
1557	11113_1.R1010	bzip(HMM:4.5e-16)
1558	363_1.R1010	bzip(HMM:4.9e-17)
1559	2733320	bzip(HMM:4e-05)
1560	1251_1.R1010	bzip(HMM:4e-05)
1561	LIB3234-037-P1-K1-B12	bzip(HMM:4e-07)
1562	12984_2.R1010	bzip(HMM:5.1e-12)
1563	120237_1.R1010	bzip(HMM:5.6e-14)
1564	640_1.R1010	bzip(HMM:5.6e-21)
1565	639_1.R1010	bzip(HMM:5.8e-24)
1566	70681_1.R1010	bzip(HMM:6.2e-09)
1567	5890_1.R1010	bzip(HMM:6e-12)
1568	5714_1.R1010	bzip(HMM:8.4e-12)
1569	jC-atXLIB327408P4a12b1	bzip(HMM:9.3e-07)
1570	30010_1.R1010	bzip(HMM:9.5e-06)
1571	24151_1.R1010	"cbfd_nfyb_hmf(HMM:0.053),histone(HMM:1e-50)"
1572	24151_2.R1010	"cbfd_nfyb_hmf(HMM:0.053),histone(HMM:4.1e-50)"
1573	9295_1.R1010	"cbfd_nfyb_hmf(HMM:0.074),histone(HMM:3.1e-47)"
1574	LIB3176-111-P1-K1-D7	"cbfd_nfyb_hmf(HMM:0.078),histone(HMM:4e-49)"
1575	751_1.R1010	cbfd_nfyb_hmf(HMM:1.2e-23)
1576	750_1.R1010	cbfd_nfyb_hmf(HMM:1.3e-21)
1577	750_2.R1010	cbfd_nfyb_hmf(HMM:1.3e-21)
1578	17669_1.R1010	cbfd_nfyb_hmf(HMM:1.6e-29)
1579	748_1.R1010	cbfd_nfyb_hmf(HMM:1e-37)
1580	749_1.R1010	cbfd_nfyb_hmf(HMM:4.9e-39)

1581	54638_1.R1010	cbfd_nfyb_hmf(HMM:5.7e-22)
1582	818_1.R1010	cbfd_nfyb_hmf(HMM:6.3e-30)
1583	LIB3176-087-P1-K1-A8	cbfd_nfyb_hmf(HMM:6e-09)
1584	4774_1.R1010	cbfd_nfyb_hmf(HMM:8e-23)
1585	LIB22-030-Q1-E1-F4	chromo(HMM:0.00065)
1586	8344_1.R1010	chromo(HMM:4.6e-19)
1587	1537_1.R1010	"csd(HMM:1.3e-21),zf-cchc(HMM:2.2e-14)"
1588	38643_1.R1010	csd(HMM:3.2e-19)
1589	1360_1.R1010	"csd(HMM:4.5e-22),zf-cchc(HMM:2.2e-14)"
1590	905705	csd(HMM:5.3e-21)
1591	22291_1.R1010	csd(HMM:6.8e-23)
1592	jC-atXLIB327425P3h08b1	dof(HMM:0.13)
1593	LIB3175-077-P1-K1-C12	dof(HMM:0.64)
1594	jC-atXLIB327417P2a09b1	dof(HMM:1 2e-35)
1595	424_1.R1010	dof(HMM:1.2e-36)
1596	16909_1.R1010	dof(HMM:1.4e-33)
1597	jC-atXLIB327410P4h02a1	dof(HMM:1.4e-34)
1598	PLN_g3386547	dof(HMM:1.4e-34)
1599	425_1.R1010	dof(HMM:1.6e-36)
1600	45689_1.R1010	dof(HMM:1.9e-34)
1601	4477_2.R1010	dof(HMM:1.9e-35)
1602	PLN_g1212758	dof(HMM:2.2e-36)
1603	63890_1.R1010	dof(HMM:2.3e-35)
1604	1800_1.R1010	dof(HMM:3.2e-35)
1605	43095_1.R1010	dof(HMM:3.5e-32)
1606	8932_1.R1010	dof(HMM:3.6e-35)
1607	1054280	dof(HMM:4.3e-35)
1608	541_2.R1010	dof(HMM:4.3e-36)
1609	541_4.R1010	dof(HMM:4.3e-36)
1610	931090	dof(HMM:4.6e-32)
1611	100709_1.R1010	dof(HMM:4.6e-36)
1612	LIB22-068-Q1-E1-C6	dof(HMM:5.1)
1613	21243_1.R1010	dof(HMM:5.1e-11)
1614	13728_1.R1010	dof(HMM:6.4e-33)
1615	5321_1.R1010	dof(HMM:6.9e-36)
1616	43095_2.R1010	dof(HMM:8.2e-32)
1617	2763897	dof(HMM:8.8e-29)
1618	LIB3234-033-P1-K1-A2	dpb(HMM:0.00035)
1619	397339	dpb(HMM:0.024)
1620	11557_3.R1010	dpb(HMM:1.5e-12)
1621	234_1.R1010	dpb(HMM:1.9e-92)
1622	52206_1.R1010	dpb(HMM:2.1e-66)
1623	jC-atXLIB327408P4a09b1	dpb(HMM:2.7e-62)
1624	2581633	dpb(HMM:3.2e-41)
1625	LIB3175-060-P1-K1-A12	dpb(HMM:3.3e-32)
1626	52206_2.R1010	dpb(HMM:3.6e-18)
1627	75516_1.R1010	dpb(HMM:4.5e-09)
1628	11557_1.R1010	dpb(HMM:5.6e-79)
1629	LIB3168-079-P1-K1-G7	enbp(HMM:1.1e-13)
1630	2445996	enbp(HMM:1 9e-10)
1631	958145	enbp(HMM:4.6e-06)
1632	LIB3234-010-P1-K1-A3	enbp(HMM:7.4e-15)

1633	5646_1.R1010	gata(HMM:0.016)
1634	82345_1.R1010	gata(HMM:0.023)
1635	1517312	gata(HMM:1.1e-14)
1636	1457_1.R1010	gata(HMM:1.1e-14)
1637	1455_1.R1010	gata(HMM:1.4e-14)
1638	1454_1.R1010	gata(HMM.1.7e-16)
1639	6981_1.R1010	gata(HMM:2.2e-08)
1640	8123_1.R1010	gata(HMM:2.2e-15)
1641	1456_1.R1010	gata(HMM.3.3e-15)
1642	61173_2.R1010	gata(HMM:3.9e-14)
1643	jC-atXP102CE2F7T7b1	gld-tea(HMM:0.00099)
1644	25183_1.R1010	gld-tea(HMM:1.1e-30)
1645	28489_1.R1010	gld-tea(HMM:1.1e-36)
1646	118662_1.R1010	gld-tea(HMM:1.7e-16)
1647	487_1.R1010	"gld-tea(HMM:1e-41),response_reg(HMM:7.4e-35)"
1648	27775_1.R1010	gld-tea(HMM:2.1e-29)
1649	PLN_g3549642	"gld-tea(HMM:2.3e-24),response_reg(HMM:3.3e-18)"
1650	934014	gld-tea(HMM:2.3e-31)
1651	18366_1.R1010	gld-tea(HMM:2.3e-32)
1652	22389_1.R1010	gld-tea(HMM:2.4e-30)
1653	2759436	gld-tea(HMM:2.6)
1654	634463	gld-tea(HMM:2.6e-30)
1655	LIB22-078-Q1-E1-G2	gld-tea(HMM:3.3e-41)
1656	52617_1.R1010	gld-tea(HMM:5.4e-37)
1657	LIB24-005-Q1-E1-F2	gld-tea(HMM:5.8e-06)
1658	266_1.R1010	"gld-tea(HMM:6.1e-43),response_reg(HMM:5.3e-34)"
1659	1401_1.R1010	gld-tea(HMM:6.4e-38)
1660	21599_1.R1010	gld-tea(HMM:8.2e-07)
1661	26342_1.R1010	gld-tea(HMM:8.4e-23)
1662	30703_1.R1010	gld-tea(HMM:8.5e-28)
1663	LIB3176-021-P1-K1-G10	gld-tea(HMM:8.7e-10)
1664	34019_1.R1010	gld-tea(HMM:8.8e-38)
1665	PLN_g3549640	"gld-tea(HMM:8.8e-38),response_reg(HMM:3.8e-38)"
1666	jC-atXP86CG9E6T7d2	"gld-tea(HMM:8.9e-19),response_reg(HMM:8.4e-36)"
1667	102479_1.R1010	gld-tea(HMM:9.2e-17)
1668	LIB3176-085-P1-K1-E8	hist_deacetyl(HMM:0.00075)
1669	78223_1.R1010	hist_deacetyl(HMM:0.0019)
1670	jC-atXP118C145L23092d2	hist_deacetyl(HMM:0.012)
1671	2764107	hist_deacetyl(HMM:0.25)
1672	17470_1.R1010	hist_deacetyl(HMM:1.4e-35)
1673	6666_1.R1010	hist_deacetyl(HMM:1.6e-16)
1674	35178_1.R1010	hist_deacetyl(HMM:1.7e-11)
1675	1576_1.R1010	hist_deacetyl(HMM:4.5e-181)
1676	LIB3234-041-P1-K1-H9	hist_deacetyl(HMM:7.7e-12)

1677	18274_1.R1010	hist_deacetyl(HMM:8.2e-18)
1678	jC-alXLIB327434P1h10a1	hist_deacetyl(HMM:9.3e-16)
1679	2758327	histone(HMM:0.0002)
1680	jC-alX24124Q1E1H01b1	histone(HMM:0.00055)
1681	jC-atX25021Q1E1G06a1	histone(HMM:0.003)
1682	LIB3176-119-P2-K1-D9	histone(HMM:0.0039)
1683	2733927	histone(HMM:0.026)
1684	LIB24-135-Q1-E1-G8	histone(HMM:0.05)
1685	jC-atXLIB327420P2a07a2	histone(HMM:0.064)
1686	2597368	histone(HMM:0.084)
1687	jC-atXLIB327413P4c02b1	histone(HMM:0.27)
1688	jC-atXLIB327429P4a06b2	histone(HMM:0.7)
1689	16709	histone(HMM:0.85)
1690	936530	histone(HMM:1.1)
1691	27124_3.R1010	histone(HMM:1.1)
1692	716_5.R1010	histone(HMM:1.1e-46)
1693	LIB25-044-Q1-E1-B10	histone(HMM:1.2)
1694	22083_3.R1010	histone(HMM:1.2e-16)
1695	LIB3175-017-P1-K1-E3	histone(HMM:1.2e-24)
1696	2612_1.R1010	histone(HMM:1.2e-43)
1697	LIB3177-019-P1-K2-B11	histone(HMM:1.3e-07)
1698	715_1.R1010	histone(HMM:1.3e-43)
1699	68_1.R1010	histone(HMM:1.3e-46)
1700	7751_1.R1010	histone(HMM:1.3e-46)
1701	716_2.R1010	histone(HMM:1.4e-31)
1702	8542_4.R1010	histone(HMM:1.4e-34)
1703	8542_2.R1010	histone(HMM:1.5e-12)
1704	1053603	histone(HMM:1.6e-27)
1705	11560_1.R1010	histone(HMM:1e-18)
1706	13777_1.R1010	histone(HMM:1e-18)
1707	13777_2.R1010	histone(HMM:1e-18)
1708	22083_1.R1010	histone(HMM:1e-18)
1709	22083_2.R1010	histone(HMM:1e-18)
1710	22083_4.R1010	histone(HMM:1e-18)
1711	LIB3176-057-P1-K1-D11	histone(HMM:1e-46)
1712	716_3.R1010	histone(HMM:1e-48)
1713	jC-atXP15C106F1T7014a1	histone(HMM:1e-48)
1714	10163_3.R1010	histone(HMM:2.1e-29)
1715	68_3.R1010	histone(HMM:2.1e-30)
1716	LIB24-095-Q1-E1-F3	histone(HMM:2.3e-07)
1717	68_6.R1010	histone(HMM:2.4e-28)
1718	11215_1.R1010	histone(HMM:2.5e-42)
1719	716_1.R1010	histone(HMM:2.5e-48)
1720	jC-atXLIB327420P2a03a2	histone(HMM:2.8e-08)
1721	LIB3176-038-P1-K1-A3	histone(HMM:2.8e-40)
1722	LIB3175-021-P1-K1-D3	histone(HMM:3.2e-24)
1723	LIB3176-027-P1-K1-F11	histone(HMM:3.8e-46)
1724	862_1.R1010	histone(HMM:3.9e-39)
1725	1217149	histone(HMM:3e-27)
1726	LIB3176-118-P2-K1-B11	histone(HMM:3e-39)
1727	LIB25-036-Q1-E1-B4	histone(HMM:4.2e-14)
1728	LIB25-057-Q1-E1-E3	histone(HMM:4.2e-14)
1729	jC-atXLIB327427P4b02a2	histone(HMM:4.7e-14)
1730	77_6.R1010	histone(HMM:4.8e-47)

1731	8542_1.R1010	histone(HMM:4.8e-47)
1732	8542_3.R1010	histone(HMM:4.8e-47)
1733	jC-atXLIB327407P1a06b2	histone(HMM:4.9e-05)
1734	68_5.R1010	histone(HMM:4e-22)
1735	LIB3175-015-P1-K1-E7	histone(HMM:5.1e-15)
1736	LIB25-102-Q1-E1-G8	histone(HMM:5.1e-17)
1737	716_6.R1010	histone(HMM:5.1e-45)
1738	27124_4.R1010	histone(HMM:5.3e-13)
1739	LIB3177-013-P1-K2-F8	histone(HMM:5.3e-19)
1740	8397_1.R1010	histone(HMM:5.3e-52)
1741	LIB25-104-Q1-E1-C11	histone(HMM:5.4e-08)
1742	LIB3177-019-P1-K1-B5	histone(HMM:5.8)
1743	10163_1.R1010	histone(HMM:5.8e-50)
1744	LIB24-125-Q1-E1-F5	histone(HMM:6.1e-05)
1745	LIB3175-033-P1-K1-A2	histone(HMM:6.2e-14)
1746	17255_1.R1010	histone(HMM:6.5e-37)
1747	jC-atXP96CH2D3T7b1	histone(HMM:6.9e-44)
1748	LIB3176-033-P1-K1-B1	histone(HMM:7.3e-25)
1749	153419_1.R1010	histone(HMM:7.6e-35)
1750	LIB3168-032-P1-K1-D3	histone(HMM:7.8e-14)
1751	13669_1.R1010	histone(HMM:8.2e-07)
1752	716_4.R1010	histone(HMM:8.3e-26)
1753	2733879	histone(HMM:8.4e-11)
1754	LIB3177-096-P1-K1-A8	histone(HMM:8.8e-19)
1755	27124_1.R1010	histone(HMM:9.5e-50)
1756	2758283	histone(HMM:9.7e-13)
1757	31420_1.R1010	hlh(HMM:0.0018)
1758	LIB3176-112-P1-K1-G6	hlh(HMM:0.0038)
1759	jC-atXB810f2	hlh(HMM:0.0055)
1760	17198_1.R1010	hlh(HMM:0.008)
1761	87116_1.R1010	hlh(HMM:0.013)
1762	117793_1.R1010	hlh(HMM:0.019)
1763	119888_1.R1010	hlh(HMM:0.025)
1764	71697_1.R1010	hlh(HMM:0.04)
1765	116704_1.R1010	hlh(HMM:0.048)
1766	jC-atXP104CE10B1T7b1	hlh(HMM:0.08)
1767	LIB24-109-Q1-E1-B3	hlh(HMM:0.092)
1768	35834_1.R1010	hlh(HMM:0.13)
1769	20469_1.R1010	hlh(HMM:1.1e-07)
1770	6545_1.R1010	hlh(HMM:1.2e-12)
1771	72703_1.R1010	hlh(HMM:1.2e-14)
1772	27829_1.R1010	hlh(HMM:1.3e-09)
1773	46829_2.R1010	hlh(HMM:1.5e-07)
1774	33631_1.R1010	hlh(HMM:2.3e-07)
1775	53493_1.R1010	hlh(HMM:2.3e-12)
1776	4019_2.R1010	hlh(HMM:2.6e-05)
1777	11026_1.R1010	hlh(HMM:2.7e-13)
1778	10361_1.R1010	hlh(HMM:2.8e-06)
1779	34071_1.R1010	hlh(HMM:3.1e-09)
1780	1520719	hlh(HMM:3.5e-09)
1781	115339_1.R1010	hlh(HMM:3.5e-09)
1782	115339_2.R1010	hlh(HMM:3.5e-09)
1783	1622_1.R1010	hlh(HMM:3.5e-15)
1784	38578_1.R1010	hlh(HMM:3.7e-09)

1785	LIB24-131-Q1-E1-G6	hlh(HMM:3e-07)
1786	349_1.R1010	hlh(HMM:4.4e-15)
1787	634586	hlh(HMM:6.7e-15)
1788	4766_1.R1010	hlh(HMM:7.1e-06)
1789	4019_3.R1010	hlh(HMM:7.3e-07)
1790	ARABL1-044-Q1-E1-D5	hlh(HMM:7.8e-05)
1791	jC-atXP123C118M3T7086a1	hlh(HMM:7.9e-12)
1792	LIB3234-048-P1-K1-B10	hlh(HMM:7e-05)
1793	1828_1.R1010	hlh(HMM:8.7e-17)
1794	32520_1.R1010	hlh(HMM:8.8e-10)
1795	jC-atXB810a2	hlh(HMM:9.3)
1796	501883	hlh(HMM:9.7)
1797	80254_1.R1010	hmg_box(HMM:0.0019)
1798	jC-alXLIB327436P3d04b1	hmg_box(HMM:0.0021)
1799	jC-atXP26C128I4T7007a1	hmg_box(HMM:0.0023)
1800	jC-atXP26C126I14T7089a1	hmg_box(HMM:0.0031)
1801	jC-atXP53C184I7T7093d1	hmg_box(HMM:0.0039)
1802	LIB3176-115-P2-K1-H1	hmg_box(HMM:0.0078)
1803	jC-atXP26C126F19T7049a1	hmg_box(HMM:0.015)
1804	16353_1.R1010	hmg_box(HMM:0.016)
1805	879_1.R1010	hmg_box(HMM:1.1e-25)
1806	876_10.R1010	hmg_box(HMM:1.2e-17)
1807	876_3.R1010	hmg_box(HMM:1.4)
1808	jC-atXP26C128L23T7016a1	hmg_box(HMM:1.6e-09)
1809	907193	hmg_box(HMM:2.5e-08)
1810	116866_1.R1010	hmg_box(HMM:2.5e-13)
1811	877_3.R1010	hmg_box(HMM:2e-28)
1812	876_5.R1010	hmg_box(HMM:3.3e-31)
1813	7619_1.R1010	hmg_box(HMM:3.8e-06)
1814	875_1.R1010	hmg_box(HMM:3.8e-30)
1815	876_1.R1010	hmg_box(HMM:3.8e-31)
1816	880_1.R1010	hmg_box(HMM:3.9e-29)
1817	jC-atXP26C124O14T7020a1	hmg_box(HMM:4.2)
1818	jC-atXP96CH2C4T7b1	hmg_box(HMM:4.7e-23)
1819	877_1.R1010	hmg_box(HMM:5.2e-33)
1820	877_2.R1010	hmg_box(HMM:5.2e-33)
1821	jC-atXP26C126K18T7090a1	hmg_box(HMM:5.4e-23)
1822	jC-atXP26C124N23T7004a1	hmg_box(HMM:6.4e-08)
1823	859_1.R1010	hmg_box(HMM:8e-20)
1824	903_1.R1010	"homeobox(HMM:0.00014),phd(HMM:4.1e-14)"
1825	1938_1.R1010	"homeobox(HMM:0.00023),homeobox_knox3(5.8e-36)"
1826	LIB3176-029-P1-K1-C6	homeobox(HMM:0.00066)
1827	515609	"homeobox(HMM:0.0048),homeobox_knox3(9.0e-13),homeobox_mat(0.0006)"
1828	990_1.R1010	"homeobox(HMM:0.008),homeobox_knox3(7.1e-22)"
1829	992_1.R1010	"homeobox(HMM:0.0082),homeobox_knox3(1.7e-21)"
1830	1362_1.R1010	"homeobox(HMM:0.0089),homeobox_knox3(1.2e-12)"
1831	991_1.R1010	"homeobox(HMM:0.011),homeo

		box_knox3(2.4e-22)"
1832	906539	"homeobox(HMM:0.016),homeo box_knox3(6.5e-23)"
1833	jC-atXLIB327408P2c09a1	"homeobox(HMM:0.036),homeo box_knox3()3.0e-10"
1834	713_1.R1010	"homeobox(HMM:0.036),homeo box_knox3(4.5e-10)"
1835	PLN_g424105	homeobox(HMM:0.054)
1836	20074_1.R1010	homeobox(HMM:0.13)
1837	987718	homeobox(HMM:0.89)
1838	24020_1.R1010	homeobox(HMM:1.1e-16)
1839	304_1.R1010	homeobox(HMM:1.2e-17)
1840	906459	homeobox(HMM:1.2e-18)
1841	13184_1.R1010	homeobox(HMM:1.2e-18)
1842	523_1.R1010	homeobox(HMM:1.4e-19)
1843	1945_1.R1010	homeobox(HMM:1.5e-17)
1844	786_1.R1010	homeobox(HMM:1.6e-20)
1845	jC-atXP65C208D10T7085d1	homeobox(HMM:1.6e-20)
1846	1548_2.R1010	homeobox(HMM:1.9e-14)
1847	LIB35-011-Q1-E1-H5	homeobox(HMM:2.1e-08)
1848	16351_1.R1010	homeobox(HMM:2.3e-18)
1849	PLN_g1694712	homeobox(HMM:2.6e-15)
1850	526_1.R1010	"homeobox(HMM:2.7e-05),homeobox_knox3(1.0e-32)"
1851	524_2.R1010	homeobox(HMM:2.9e-11)
1852	12540_1.R1010	homeobox(HMM:2e-15)
1853	1517240	homeobox(HMM:3.4e-14)
1854	787_6.R1010	homeobox(HMM:3.5e-19)
1855	PLN_g16333	homeobox(HMM:3.5e-19)
1856	PLN_g16325	"homeobox(HMM:4.2e-05),phd(HMM:5.4e-14)"
1857	786_5.R1010	homeobox(HMM:4.2e-11)
1858	9463_1.R1010	homeobox(HMM:4.3e-13)
1859	307_1.R1010	homeobox(HMM:4.3e-15)
1860	525_1.R1010	homeobox(HMM:4.6e-18)
1861	6707_1.R1010	homeobox(HMM:4.7)
1862	524_1.R1010	homeobox(HMM:4.8e-19)
1863	69_1.R1010	homeobox(HMM:4e-16)
1864	PLN_g16178	homeobox(HMM:4e-16)
1865	1433_1.R1010	homeobox(HMM:5.1e-20)
1866	306_1.R1010	homeobox(HMM:5.5e-15)
1867	305_1.R1010	homeobox(HMM:6.4e-15)
1868	63323_1.R1010	homeobox(HMM:7.7e-18)
1869	786_3.R1010	homeobox(HMM:7.8e-16)
1870	jC-atXP112C132D23T7a1	homeobox(HMM:8.7e-14)
1871	jC-atXP82CG2G3T7d3	homeobox_knox3(3.9e-27)
1872	LIB3176-040-P1-K1-F6	homeobox_knox3(4.6e-07)
1873	1268568	homeobox_knox3(9.4e-13)
1874	2759253	hsf_dna-bind(HMM:0.28)
1875	2996_1.R1010	hsf_dna-bind(HMM:1.1e-22)
1876	944_1.R1010	hsf_dna-bind(HMM:1.2e-65)
1877	119770_1.R1010	hsf_dna-bind(HMM:1.5e-39)
1878	jC-atXP124C125H21T7d1	hsf_dna-bind(HMM:1.6e-11)
1879	13823_1.R1010	hsf_dna-bind(HMM:1e-36)

1880	268_1.R1010	hsf_dna-bind(HMM:2.6e-98)
1881	PLN_g3256067	hsf_dna-bind(HMM:3.3e-89)
1882	5332_1.R1010	hsf_dna-bind(HMM:6.4e-39)
1883	30824_1 R1010	hsf_dna-bind(HMM:8.1e-52)
1884	957701	hsf_dna-bind(HMM:9.9e-06)
1885	32489_1.R1010	hsf_dna-bind(HMM:9e-12)
1886	11068_1.R1010	iaa(HMM:0.0001)
1887	67079_1.R1010	iaa(HMM:0.00017)
1888	jC-atXP66C210I12T7005a1	iaa(HMM:0.0002)
1889	2122_2.R1010	iaa(HMM:0.00027)
1890	jC-atXLIB327433P2a08a1	iaa(HMM:0.00032)
1891	18819_1.R1010	iaa(HMM:0.00095)
1892	jC-atXP102CE3H6T7b1	iaa(HMM:0.0037)
1893	80560_1 R1010	iaa(HMM:0.0062)
1894	4542_1.R1010	iaa(HMM:0.034)
1895	2581617	iaa(HMM:0.041)
1896	ARABL1-027-Q1-B1-E5	iaa(HMM:0.068)
1897	1980_2.R1010	iaa(HMM:0.075)
1898	623623	iaa(HMM:0.083)
1899	1829_1.R1010	iaa(HMM:1.1e-51)
1900	25194_1 R1010	iaa(HMM:1.2e-08)
1901	183_2.R1010	iaa(HMM:1.4e-54)
1902	LIB3177-097-P1-K1-D6	iaa(HMM:1.5e-15)
1903	1980_1.R1010	iaa(HMM:1.5e-69)
1904	123277_1.R1010	iaa(HMM:1.6e-19)
1905	1827_1.R1010	iaa(HMM:1.6e-68)
1906	PLN_g16198	iaa(HMM:1.7e-51)
1907	LIB3176-041-P1-K1-A5	iaa(HMM:1.9e-15)
1908	2122_1.R1010	iaa(HMM:1e-45)
1909	jC-atXLIB327412P4c02b1	iaa(HMM:1e-45)
1910	45287_1.R1010	iaa(HMM:1e-51)
1911	jC-atXP4C88I23T7076a1	iaa(HMM:2.1e-28)
1912	PLN_g972932	iaa(HMM:2.6e-09)
1913	32268_1.R1010	iaa(HMM:2e-09)
1914	2581664	iaa(HMM:3.1e-21)
1915	78392_1.R1010	iaa(HMM:3.1e-61)
1916	jC-atXLIB327411P1f02a1	iaa(HMM:3.4e-44)
1917	183_3.R1010	iaa(HMM:3.4e-58)
1918	25194_2.R1010	iaa(HMM:3.5e-45)
1919	jC-atXP60C198O12T7040d1	iaa(HMM:4.3e-12)
1920	59298_1.R1010	iaa(HMM:4.4e-18)
1921	61018_1.R1010	iaa(HMM:4.7e-07)
1922	jC-atXP71C222G9T7s2	iaa(HMM:6.1e-05)
1923	23678_1.R1010	iaa(HMM:6.9e-69)
1924	210_1.R1010	iaa(HMM:6e-65)
1925	54_1.R1010	iaa(HMM:7.1e-61)
1926	jC-atXLIB327414P2b04a1	iaa(HMM:7.7e-05)
1927	8884_1.R1010	iaa(HMM:9.3e-66)
1928	LIB3177-048-P1-K1-C12	iaa(HMM:9.8e-10)
1929	LIB24-080-Q1-E1-D11	ibr(HMM:6.6e-05)
1930	906045	k-box(HMM:0.0013)
1931	906457	"k-box(HMM 0.0081),srf-tf(HMM 2.5e-16)"
1932	103229_2.R1010	k-box(HMM:1.3e-23)

1933	PLN_g3719214	"k-box(HMM:1.3e-23),srf-tf(HMM:5.9e-34)"
1934	PLN_g1737494	"k-box(HMM:1.5e-32),srf-tf(HMM:1.7e-37)"
1935	1917_1.R1010	"k-box(HMM:1.5e-37),srf-tf(HMM:1.3e-37)"
1936	jC-atX22033Q1E2A09a1	k-box(HMM:1.6)
1937	1583_1.R1010	"k-box(HMM:1.6e-39),srf-tf(HMM:7.5e-38)"
1938	508_1.R1010	"k-box(HMM:1.6e-42),srf-tf(HMM:8.5e-37)"
1939	738_1.R1010	"k-box(HMM:1.7e-41),srf-tf(HMM:7.5e-38)"
1940	740_3.R1010	"k-box(HMM:1.8e-06),srf-tf(HMM:5.1e-36)"
1941	PLN_g1019924	"k-box(HMM:1.9e-38),srf-tf(HMM:2.9e-38)"
1942	871_1.R1010	"k-box(HMM:1e-28),srf-tf(HMM:1.1e-33)"
1943	752_1.R1010	"k-box(HMM:1e-28),srf-tf(HMM:2.4e-37)"
1944	740_2.R1010	"k-box(HMM:2.1e-15),srf-tf(HMM:5.1e-36)"
1945	8965_1.R1010	"k-box(HMM:2.2e-13),srf-tf(HMM:7.6e-36)"
1946	1351_1.R1010	"k-box(HMM:3.4e-41),srf-tf(HMM:2.8e-37)"
1947	906325	k-box(HMM:3.6e-18)
1948	PLN_g862641	"k-box(HMM:3.6e-32),srf-tf(HMM:1.8e-35)"
1949	2747387	"k-box(HMM:4.5),srf-tf(HMM:1.1e-33)"
1950	1216678	k-box(HMM:5.1e-15)
1951	1871_1.R1010	"k-box(HMM:5.2e-11),srf-tf(HMM:5.1e-32)"
1952	740_1.R1010	"k-box(HMM:5.6e-43),srf-tf(HMM:5.6e-36)"
1953	1919_1.R1010	"k-box(HMM:5e-24),srf-tf(HMM:2.6e-32)"
1954	2747374	"k-box(HMM:6.2),srf-tf(HMM:5e-37)"
1955	504_1.R1010	"k-box(HMM:6.7e-25),srf-tf(HMM:5.5e-36)"
1956	119869_1.R1010	k-box(HMM:6.9e-06)
1957	jC-atXLIB327408P1d08b1	"k-box(HMM:6.9e-15),srf-tf(HMM:8.1e-35)"
1958	739_1.R1010	"k-box(HMM:7.7e-40),srf-tf(HMM:1.1e-37)"
1959	14225_1.R1010	"k-box(HMM:8.3e-06),srf-tf(HMM:1.5e-27)"
1960	8965_3.R1010	k-box(HMM:8.5e-13)
1961	jC-atXLIB327423P2e10b1	keyword:14-3-3(1.0e-10)
1962	jC-atXLIB327424P1b02a1	keyword:14-3-3(1.0e-155)
1963	LIB25-093-Q1-E1-E6	keyword:14-3-3(1.0e-76)

1964	jC-atXLIB327413P3f01b1	keyword:14-3-3(2.0e-37)
1965	jC-atXLIB327413P4g01a1	keyword:14-3-3(2.0e-56)
1966	jC-atXLIB327409P4c08a1	keyword:AGAMOUS(7.0e-30)
1967	ARABL1-032-Q1-E1-B3	keyword:AGL(1.0e-125)
1968	ARABL1-031-Q1-E1-G9	keyword:AGL(2.0e-14)
1969	ARABL1-031-Q1-E1-B12	keyword:AGL(4.0e-34)
1970	12865_1.R1010	keyword:AGL(6.0e-41)
1971	935541	keyword:ap2(0.0e+00)
1972	132752_1.R1010	keyword:ap2(0.0e+00)
1973	419_1.R1010	keyword:ap2(0.0e+00)
1974	4655_1.R1010	keyword:ap2(0.0e+00)
1975	3449953	keyword:ap2(1.0e-08)
1976	LIB22-004-Q1-E1-D12	keyword:ap2(1.0e-16)
1977	3450179	keyword:ap2(1.0e-170)
1978	5199_2.R1010	keyword:ap2(1.0e-20)
1979	LIB3176-022-P1-K1-F12	keyword:ap2(1.0e-25)
1980	jC-atXLIB327416P3g11b1	keyword:ap2(1.0e-78)
1981	jC-atXP89CG6A8T7092d1	keyword:ap2(2.0e-14)
1982	jC-atXLIB327434P2c11a1	keyword:ap2(2.0e-22)
1983	2749550	keyword:ap2(2.0e-33)
1984	77044_1.R1010	keyword:ap2(2.0e-34)
1985	496444	keyword:ap2(2.0e-66)
1986	5255_1.R1010	keyword:ap2(2.0e-77)
1987	4590_1.R1010	keyword:ap2(2.0e-81)
1988	LIB3175-077-P1-K1-F9	keyword:ap2(3.0e-25)
1989	2393175	keyword:ap2(3.0e-34)
1990	jC-atXP66C210C17T7011a1	keyword:ap2(3.0e-51)
1991	470_5.R1010	keyword:ap2(3.0e-52)
1992	2218_1.R1010	keyword:ap2(3.0e-57)
1993	jC-atXLIB327413P2a08b1	keyword:ap2(3.0e-67)
1994	jC-atXP83C241K21T7050a1	keyword:ap2(4.0e-09)
1995	jC-atXP53C185C24T7023d1	keyword:ap2(4.0e-17)
1996	LIB22-071-Q1-E1-A2	keyword:ap2(4.0e-39)
1997	501884	keyword:ap2(4.0e-50)
1998	jC-atXLIB327432P4f01a1	keyword:ap2(6.0e-25)
1999	jC-atXLIB327440P3e04a1	keyword:ap2(6.0e-35)
2000	2218_2.R1010	keyword:ap2(7.0e-27)
2001	2393624	keyword:ap2(7.0e-42)
2002	91510_1.R1010	keyword:ap2(8.0e-33)
2003	5715_2.R1010	keyword:ap2(8.0e-77)
2004	jC-atXP6C90J5T7s1	keyword:ap2(9.0e-43)
2005	467_1.R1010	keyword:AT-hook(1.0e-172)
2006	LIB22-063-Q1-E1-C11	keyword:AT-hook(1.0e-25)
2007	jC-atXLIB327404P4a08b1	keyword:AT-hook(1.0e-40)
2008	LIB3176-027-P1-K1-C11	keyword:AT-hook(3.0e-16)
2009	1318_1.R1010	keyword:bzip(0.0e+00)
2010	jC-atXLIB327407P1g04a2	"keyword:bzip(1.0e-17),keyword:homeobox(1.0e-17)"
2011	21876_1.R1010	keyword:bzip(1.0e-31)
2012	905603	keyword:bzip(1.0e-53)
2013	1053939	keyword:bzip(1.0e-55)
2014	38177_1.R1010	keyword:bzip(1.0e-61)
2015	402964	keyword:bzip(2.0e-13)

2016	jC-atXLIB327410P4h11a1	"keyword:bzip(2.0e-35),keyword:homeobox(2.0e-35)"
2017	LIB24-064-Q1-E1-G3	keyword:bzip(2.0e-43)
2018	LIB22-009-Q1-E1-D7	"keyword:bzip(2.0e-46),keyword:homeobox(2.0e-46)"
2019	LIB3234-041-P1-K1-H6	keyword:bzip(2.0e-53)
2020	jC-atXLIB327424P4g06b1	keyword:bzip(3.0e-19)
2021	jC-atXLIB327439P2f05a2	"keyword:bzip(3.0e-19),keyword:homeobox(3.0e-19)"
2022	1318_2.R1010	keyword:bzip(3.0e-24)
2023	LIB3234-048-P1-K1-F4	keyword:bzip(3.0e-32)
2024	94252_2.R1010	"keyword:bzip(3.0e-62),keyword:homeobox(3.0e-62)"
2025	jC-atXLIB327430P2h03a1	"keyword:bzip(4.0e-11),keyword:homeobox(4.0e-11)"
2026	402959	keyword:bzip(4.0e-66)
2027	jC-atXLIB327404P4f06a1	keyword:bzip(6.0e-24)
2028	jC-atX24066Q1E1D09b1	keyword:bzip(6.0e-42)
2029	LIB24-083-Q1-E1-C4	keyword:bzip(7.0e-31)
2030	94252_1.R1010	"keyword:bzip(7.0e-71),keyword:homeobox(7.0e-71)"
2031	29979_1.R1010	keyword:bzip(7.0e-98)
2032	56920_1.R1010	keyword:CONSTANS(1.0e-136)
2033	jC-atXLIB327432P4g06a1	keyword:CONSTANS(1.0e-17)
2034	84391_1.R1010	keyword:CONSTANS(1.0e-178)
2035	2750018	keyword:CONSTANS(1.0e-57)
2036	21891_1.R1010	keyword:CONSTANS(2.0e-15)
2037	jC-atXLIB327416P2e02a1	keyword:CONSTANS(2.0e-23)
2038	jC-atXLIB327416P2e02b1	keyword:CONSTANS(2.0e-71)
2039	jC-atXLIB327416P4e05b1	keyword:CONSTANS(2.0e-74)
2040	84077_1.R1010	keyword:CONSTANS(3.0e-35)
2041	394825	keyword:CONSTANS(4.0e-09)
2042	13864_1.R1010	keyword:CONSTANS(5.0e-25)
2043	15277_1.R1010	keyword:CONSTANS(5.0e-32)
2044	84077_3.R1010	keyword:CONSTANS(9.0e-25)
2045	1420_1.R1010	keyword:dna-binding(0.0e+00)
2046	3546_2.R1010	keyword:dna-binding(0.0e+00)
2047	24889_3.R1010	keyword:dna-binding(1.0e-08)
2048	54355_1.R1010	keyword:dna-binding(1.0e-09)
2049	jC-alXLIB327434P3b03b1	keyword:dna-binding(1.0e-102)
2050	315534	keyword:dna-binding(1.0e-11)
2051	jC-atXLI13Q1B1C08b1	keyword:dna-binding(1.0e-12)
2052	jC-atXLIB327418P3e11a2	keyword:dna-binding(1.0e-18)
2053	jC-atXP118C155O7T7096a1	keyword:dna-binding(1.0e-20)
2054	LIB22-045-Q1-E1-A8	keyword:dna-binding(1.0e-20)
2055	LIB3176-009-P1-K2-E12	keyword:dna-binding(1.0e-32)
2056	50530_1.R1010	keyword:dna-binding(1.0e-37)
2057	33009_1.R1010	keyword:dna-binding(1.0e-39)

2058	4524_1.R1010	keyword:dna-binding(1.0e-43)
2059	36029_1.R1010	keyword:dna-binding(1.0e-45)
2060	315971	keyword:dna-binding(1.0e-47)
2061	jC-atXP122C120F1T7052a1	keyword:dna-binding(1.0e-47)
2062	119764_1.R1010	keyword:dna-binding(1.0e-50)
2063	LIB24-001-Q1-E1-F8	keyword:dna-binding(1.0e-53)
2064	84130_1.R1010	keyword:dna-binding(2.0e-10)
2065	jC-atXP15C106F5T7d1	keyword:dna-binding(2.0e-11)
2066	jC-atXLIB327416P3h10b1	keyword:dna-binding(2.0e-12)
2067	LIB146-006-Q1-E1-A10	keyword:dna-binding(2.0e-23)
2068	LIB3177-088-P1-K1-C2	keyword:dna-binding(2.0e-25)
2069	2048226	keyword:dna-binding(2.0e-26)
2070	LIB3168-045-P1-K1-F9	keyword:dna-binding(2.0e-31)
2071	LIB3175-024-P1-K1-F6	keyword:dna-binding(2.0e-40)
2072	28466_1.R1010	keyword:dna-binding(2.0e-41)
2073	12312_3.R1010	keyword:dna-binding(2.0e-56)
2074	49568_1.R1010	keyword:dna-binding(2.0e-67)
2075	72470_1.R1010	keyword:dna-binding(2.0e-75)
2076	jC-atXP32C147L20T7d2	keyword:dna-binding(2.0e-98)
2077	jC-atXP20C115I5T7095a1	keyword:dna-binding(3.0e-09)
2078	115981_1.R1010	keyword:dna-binding(3.0e-11)
2079	LIB3176-101-P1-K1-A8	keyword:dna-binding(3.0e-14)
2080	33537_1.R1010	keyword:dna-binding(3.0e-21)
2081	LIB3175-029-P1-K1-H1	keyword:dna-binding(3.0e-29)
2082	22735_1.R1010	keyword:dna-binding(3.0e-37)
2083	2597524	keyword:dna-binding(3.0e-46)
2084	LIB3168-050-P1-K1-B3	keyword:dna-binding(3.0e-76)
2085	12312_1.R1010	keyword:dna-binding(4.0e-15)
2086	31356_1.R1010	keyword:dna-binding(4.0e-19)
2087	jC-atXLIB327432P3d03a1	keyword:dna-binding(4.0e-50)
2088	12312_2.R1010	keyword:dna-binding(4.0e-53)
2089	12570_1.R1010	keyword:dna-binding(4.0e-56)
2090	2413873	keyword:dna-binding(5.0e-09)
2091	jC-alX24092Q1E1A05a1	keyword:dna-binding(5.0e-14)
2092	jC-atXLIB327428P1h11b2	keyword:dna-binding(5.0e-26)
2093	12570_3.R1010	keyword:dna-binding(5.0e-49)
2094	LIB3175-019-P1-K1-D10	keyword:dna-binding(5.0e-51)
2095	12570_4.R1010	keyword:dna-binding(6.0e-18)
2096	jC-atXLIB327417P2e01a1	keyword:dna-binding(6.0e-29)
2097	116933_1.R1010	keyword:dna-binding(6.0e-39)
2098	12570_2.R1010	keyword:dna-binding(6.0e-60)
2099	jC-atXP32C147M6T7d2	keyword:dna-binding(6.0e-84)
2100	3450011	keyword:dna-binding(6.0e-86)
2101	2596745	keyword:dna-binding(7.0e-25)
2102	24889_1.R1010	keyword:dna-binding(7.0e-29)
2103	LIB3175-037-P1-K1-B1	keyword:dna-binding(8.0e-20)
2104	jC-atXLIB327424P1b01a1	keyword:dna-binding(8.0e-46)
2105	905518	keyword:dna-binding(8.0e-56)
2106	jC-atXLIB327407P3g01b1	keyword:dna-binding(9.0e-14)
2107	2748159	keyword:dna-binding(9.0e-15)
2108	LIB3177-019-P1-K1-B4	keyword:dna-binding(9.0e-22)
2109	LIB23-006-Q1-E1-F3	keyword:dna-binding(9.0e-53)
2110	LIB24-013-Q1-E1-E4	keyword:enbp(2.0e-27)
2111	80146_1.R1010	keyword:helix-loop-helix(1.0e-

		51)
2112	jC-atXP71C221K10T7s2	"keyword:helix-loop-helix(1.0e-51),keyword:dna-binding(1.0e-51)"
2113	29033_2.R1010	"keyword:helix-loop-helix(2.0e-16),keyword:dna-binding(2.0e-16)"
2114	24208_1.R1010	"keyword:helix-loop-helix(3.0e-35),keyword:dna-binding(3.0e-35)"
2115	29033_1.R1010	"keyword:helix-loop-helix(3.0e-56),keyword:dna-binding(3.0e-56)"
2116	27932_1.R1010	keyword:homeobox(1.0e-100)
2117	8022_1.R1010	keyword:homeobox(1.0e-104)
2118	jC-atXLIB327421P4f06b1	"keyword:homeobox(1.0e-14),keyword:homeodomain(1.0e-14)"
2119	jC-atXLIB327427P2a01b1	"keyword:homeobox(1.0e-20),keyword:Leucine-zipper(1.0e-20)"
2120	jC-atXLIB327412P1h09b1	keyword:homeobox(1.0e-28)
2121	787_3.R1010	keyword:homeobox(1.0e-31)
2122	LIB3175-052-P1-K1-E12	keyword:homeobox(1.0e-66)
2123	2763037	"keyword:homeobox(2.0e-14),keyword:Leucine-zipper(2.0e-14)"
2124	jC-atXLIB327412P1f09b1	"keyword:homeobox(2.0e-19),keyword:Leucine-zipper(2.0e-19)"
2125	4534_1.R1010	keyword:homeobox(2.0e-33)
2126	524_3.R1010	"keyword:homeobox(2.0e-36),keyword:Leucine-zipper(2.0e-36)"
2127	937_3.R1010	keyword:homeobox(2.0e-94)
2128	32367_1.R1010	keyword:homeobox(3.0e-09)
2129	jC-atXP31C147D12T7d2	keyword:homeobox(3.0e-48)
2130	991_3.R1010	keyword:homeobox(3.0e-88)
2131	63944_1.R1010	keyword:homeobox(3.0e-99)
2132	932917	"keyword:homeobox(4.0e-14),keyword:Leucine-zipper(4.0e-14)"
2133	LIB23-026-Q1-E1-A2	keyword:homeobox(4.0e-49)
2134	41720_1.R1010	"keyword:homeobox(4.0e-65),keyword:homeodomain(4.0e-65)"
2135	jC-atXLIB327421P2c04b1	"keyword:homeobox(5.0e-09),keyword:Leucine-zipper(5.0e-09)"
2136	jC-atXP82CG2G3T7b1	keyword:homeobox(5.0e-88)
2137	46458_1.R1010	"keyword:homeobox(6.0e-09),keyword:Leucine-zipper(6.0e-09)"
2138	88865_1.R1010	"keyword:homeobox(6.0e-

		34),keyword:Leucine-zipper(6.0e-34)"
2139	LIB3176-033-P1-K1-F7	keyword:homeobox(6.0e-39)
2140	LIB3175-034-P1-K1-H4	keyword:homeobox(6.0e-62)
2141	LIB3168-070-P1-K1-B5	keyword:homeobox(7.0e-29)
2142	51177_1.R1010	"keyword:homeobox(7.0e-47),keyword:Leucine-zipper(7.0e-47)"
2143	11171_1.R1010	keyword:homeobox(7.0e-74)
2144	LIB3176-054-P1-K1-A8	keyword:homeobox(8.0e-36)
2145	56378_1.R1010	keyword:homeobox(8.0e-75)
2146	2048209	"keyword:homeobox(9.0e-42),keyword:Leucine-zipper(9.0e-42)"
2147	1269190	keyword:homeobox(9.0e-47)
2148	jC-atXLIB327403P1c08b1	keyword:homeodomain(1.0e-10)
2149	66256_1.R1010	keyword:homeodomain(1.0e-11)
2150	1216646	keyword:homeodomain(1.0e-41)
2151	17808_1.R1010	keyword:homeodomain(1.0e-44)
2152	66895_1.R1010	keyword:homeodomain(1.0e-49)
2153	LIB3175-004-P1-K1-E7	keyword:homeodomain(2.0e-09)
2154	LIB3234-054-P1-K1-F12	keyword:homeodomain(2.0e-09)
2155	129896_1.R1010	keyword:homeodomain(2.0e-12)
2156	LIB3168-035-P1-K1-H3	keyword:homeodomain(2.0e-22)
2157	8758_1.R1010	keyword:homeodomain(2.0e-31)
2158	903_2.R1010	keyword:homeodomain(2.0e-72)
2159	jC-atXLIB327406P4d02b2	keyword:homeodomain(3.0e-24)
2160	LIB25-029-Q1-E1-F1	keyword:homeodomain(3.0e-34)
2161	935428	keyword:homeodomain(3.0e-51)
2162	4654_1.R1010	keyword:homeodomain(3.0e-56)
2163	13187_1.R1010	keyword:homeodomain(4.0e-23)
2164	46464_1.R1010	keyword:homeodomain(4.0e-64)
2165	2597358	keyword:homeodomain(5.0e-11)
2166	6659_1.R1010	keyword:homeodomain(5.0e-27)
2167	LIB3175-044-P1-K1-E2	keyword:Leucine-zipper(4.0e-13)
2168	LIB3168-005-P1-K1-G3	keyword:Leucine-zipper(5.0e-25)
2169	2749526	"keyword:mads(3.0e-09),keyword:AGL(3.0e-09)"
2170	jC-atXP62C201N18T7020a1	"keyword:mads(7.0e-17),keyword:AGL(7.0e-17)"
2171	744_1.R1010	keyword:myb(0.0e+00)
2172	LIB3176-020-P1-K1-B9	keyword:myb(1.0e-10)
2173	22467_1.R1010	keyword:myb(1.0e-63)
2174	30118_1.R1010	"keyword:myb(2.0e-11),keyword:dna-binding(2.0e-11)"
2175	LIB3177-038-P1-K1-B12	"keyword:myb(2.0e-15),keyword:dna-binding(2.0e-15)"
2176	jC-atXLIB327421P3e08b1	keyword:myb(2.0e-19)
2177	28031_1.R1010	keyword:myb(2.0e-28)
2178	147359_1.R1010	keyword:myb(3.0e-43)
2179	LIB35-011-Q1-E1-A10	"keyword:myb(4.0e-10),keyword:dna-binding(4.0e-

		10)"
2180	LIB3176-001-Q1-K1-E8	"keyword:myb(5.0e-15),keyword:dna-binding(5.0e-15)"
2181	LIB3234-020-P1-K1-D4	"keyword:myb(5.0e-17),keyword:dna-binding(5.0e-17)"
2182	LIB35-042-Q1-E1-B7	keyword:myb(8.0e-38)
2183	152400_1.R1010	keyword:myb(9.0e-52)
2184	2048440	keyword:scarecrow(1.0e-114)
2185	2714_1.R1010	keyword:scarecrow(1.0e-128)
2186	757676	keyword:scarecrow(1.0e-45)
2187	LIB22-035-Q1-E1-F9	keyword:scarecrow(1.0e-56)
2188	75150_1.R1010	keyword:scarecrow(2.0e-22)
2189	59776_2.R1010	keyword:scarecrow(2.0e-32)
2190	jC-alX25092Q1E1A12a1	keyword:scarecrow(2.0e-35)
2191	117936_1.R1010	keyword:scarecrow(2.0e-63)
2192	34737_2.R1010	keyword:scarecrow(3.0e-27)
2193	jC-atXP10C95M21T7s1	keyword:scarecrow(3.0e-59)
2194	jC-atXP113C229C9T7064a1	keyword:scarecrow(4.0e-13)
2195	jC-atXLIB327428P4d10b1	keyword:scarecrow(4.0e-14)
2196	135199_1.R1010	keyword:scarecrow(5.0e-12)
2197	jC-atXLIB327407P4b10a1	keyword:scarecrow(5.0e-13)
2198	LIB25-017-Q1-E1-A10	keyword:scarecrow(5.0e-32)
2199	12191_1.R1010	keyword:scarecrow(5.0e-59)
2200	7235_1.R1010	keyword:scarecrow(7.0e-42)
2201	jC-atXLIB327426P4b12a1	keyword:scarecrow(8.0e-10)
2202	115767_1.R1010	keyword:scarecrow(8.0e-41)
2203	jC-atXLIB327432P1f04a1	keyword:scarecrow(9.0e-24)
2204	135411_1.R1010	keyword:scarecrow(9.0e-26)
2205	3450092	keyword:transcription(0.0e+00)
2206	jC-atX24106Q1E1F08a1	keyword:transcription(0.0e+00)
2207	3450242	"keyword:transcription(0.0e+00), keyword:myb(0.0e+00)"
2208	9130_1.R1010	"keyword:transcription(1.0e-08),keyword:myb(1.0e-08)"
2209	jC-atXLIB327423P2e07a1	"keyword:transcription(1.0e-08),keyword:myb(1.0e-08)"
2210	125586_1.R1010	keyword:transcription(1.0e-09)
2211	LIB3177-089-P1-K1-A2	keyword:transcription(1.0e-09)
2212	75270_1.R1010	keyword:transcription(1.0e-10)
2213	LIB3168-018-P1-K1-G10	keyword:transcription(1.0e-10)
2214	jC-atXLIB327402P1h08b1	"keyword:transcription(1.0e-10),keyword:myb(1.0e-10)"
2215	jC-atXLIB327407P1b02b1	"keyword:transcription(1.0e-10),keyword:myb(1.0e-10)"
2216	jC-atXLIB327407P2f05b1	"keyword:transcription(1.0e-10),keyword:myb(1.0e-10)"
2217	jC-atXLIB327422P1e12b1	"keyword:transcription(1.0e-10),keyword:myb(1.0e-10)"
2218	jC-atXLIB327439P2a04b2	"keyword:transcription(1.0e-10),keyword:myb(1.0e-10)"
2219	jC-atXP11C97O20T7027d1	"keyword:transcription(1.0e-10),keyword:myb(1.0e-10)"

2220	7033_3.R1010	keyword:transcription(1.0e-100)
2221	5416_2.R1010	keyword:transcription(1.0e-102)
2222	23652_1.R1010	"keyword:transcription(1.0e-103),keyword:helix-loop-helix(1.0e-103)"
2223	33416_1.R1010	"keyword:transcription(1.0e-107),keyword:myb(1.0e-107)"
2224	LIB3234-026-Q1-K1-H11	"keyword:transcription(1.0e-11),keyword:bzip(1.0e-11)"
2225	129514_1.R1010	"keyword:transcription(1.0e-11),keyword:myb(1.0e-11)"
2226	41112_1.R1010	"keyword:transcription(1.0e-11),keyword:myb(1.0e-11)"
2227	jC-atXP109C99M15T7s1	"keyword:transcription(1.0e-11),keyword:myb(1.0e-11)"
2228	60749_1.R1010	keyword:transcription(1.0e-110)
2229	jC-atXP60C199J4T7044d1	"keyword:transcription(1.0e-12),keyword:myb(1.0e-12)"
2230	jC-atXP65C209F6T7072d1	"keyword:transcription(1.0e-12),keyword:myb(1.0e-12)"
2231	1464_1.R1010	keyword:transcription(1.0e-129)
2232	30041_1.R1010	"keyword:transcription(1.0e-13),keyword:myb(1.0e-13)"
2233	jC-atXLIB327407P2a05b1	"keyword:transcription(1.0e-13),keyword:myb(1.0e-13)"
2234	jC-atXLIB327407P2b06b1	"keyword:transcription(1.0e-13),keyword:myb(1.0e-13)"
2235	jC-atXLIB327432P2h05b2	"keyword:transcription(1.0e-13),keyword:myb(1.0e-13)"
2236	jC-atXP69C219L23T7039d1	"keyword:transcription(1.0e-13),keyword:myb(1.0e-13)"
2237	745_1.R1010	keyword:transcription(1.0e-135)
2238	jC-atXLIB327408P2d04a1	keyword:transcription(1.0e-14)
2239	2753_1.R1010	"keyword:transcription(1.0e-14),keyword:bzip(1.0e-14)"
2240	27966_1.R1010	keyword:transcription(1.0e-15)
2241	73496_1.R1010	keyword:transcription(1.0e-16)
2242	jC-atXP70C222C9T7008a1	keyword:transcription(1.0e-16)
2243	112604_1.R1010	"keyword:transcription(1.0e-16),keyword:bzip(1.0e-16)"
2244	746_1.R1010	keyword:transcription(1.0e-160)
2245	LIB24-115-Q1-E1-A9	"keyword:transcription(1.0e-160),keyword:AGL(1.0e-160)"
2246	2749226	"keyword:transcription(1.0e-171),keyword:myb(1.0e-171)"
2247	484_1.R1010	keyword:transcription(1.0e-178)
2248	747_1.R1010	keyword:transcription(1.0e-180)
2249	LIB3177-022-P1-K2-A6	keyword:transcription(1.0e-19)
2250	jC-atXLIB327413P3d05b1	"keyword:transcription(1.0e-19),keyword:myb(1.0e-19)"
2251	jC-atXLIB327422P3a10b2	"keyword:transcription(1.0e-19),keyword:myb(1.0e-19)"
2252	2581653	keyword:transcription(1.0e-22)
2253	jC-atX22004Q1E1E06a1	keyword:transcription(1.0e-23)

2254	LIB3168-026-P1-K1-H8	keyword:transcription(1.0e-23)
2255	957807	keyword:transcription(1.0e-32)
2256	LIB22-016-Q1-E1-G1	keyword:transcription(1.0e-37)
2257	LIB3175-038-P1-K1-E2	keyword:transcription(1.0e-37)
2258	484_2.R1010	keyword:transcription(1.0e-38)
2259	jC-atXLIB327410P1h01b1	keyword:transcription(1.0e-38)
2260	2965_1.R1010	keyword:transcription(1.0e-41)
2261	5417_1.R1010	keyword:transcription(1.0e-44)
2262	1454_2.R1010	keyword:transcription(1.0e-47)
2263	LIB25-021-Q1-E1-F6	"keyword:transcription(1.0e-51),keyword:AGL(1.0e-51)"
2264	483_1.R1010	keyword:transcription(1.0e-54)
2265	2413903	keyword:transcription(1.0e-59)
2266	135726_1.R1010	keyword:transcription(1.0e-60)
2267	4173_2.R1010	keyword:transcription(1.0e-60)
2268	LIB146-006-Q1-E1-D8	"keyword:transcription(1.0e-67),keyword:myb(1.0e-67)"
2269	24872_1.R1010	keyword:transcription(1.0e-68)
2270	5362_1.R1010	keyword:transcription(1.0e-68)
2271	jC-atXP7C91N10T7s1	"keyword:transcription(1.0e-80),keyword:myb(1.0e-80)"
2272	126613_1.R1010	keyword:transcription(1.0e-81)
2273	117821_1.R1010	keyword:transcription(2.0e-09)
2274	jC-atXP70C222C6T7087a1	keyword:transcription(2.0e-09)
2275	33875_1.R1010	"keyword:transcription(2.0e-09),keyword:dna-binding(2.0e-09)"
2276	jC-atXLIB327406P3b03b2	"keyword:transcription(2.0e-09),keyword:myb(2.0e-09)"
2277	jC-atXLIB327424P3h02b1	"keyword:transcription(2.0e-09),keyword:myb(2.0e-09)"
2278	jC-atXLIB327432P2h07b2	"keyword:transcription(2.0e-09),keyword:myb(2.0e-09)"
2279	23953_1.R1010	"keyword:transcription(2.0e-10),keyword:myb(2.0e-10)"
2280	jC-atXLIB327401P4c03b2	"keyword:transcription(2.0e-10),keyword:myb(2.0e-10)"
2281	jC-atXLIB327412P1a12b1	"keyword:transcription(2.0e-11),keyword:myb(2.0e-11)"
2282	jC-atXLIB327422P3h11b2	"keyword:transcription(2.0e-11),keyword:myb(2.0e-11)"
2283	40610_1.R1010	keyword:transcription(2.0e-12)
2284	LIB25-036-Q1-E1-B11	keyword:transcription(2.0e-12)
2285	24234_1.R1010	"keyword:transcription(2.0e-12),keyword:myb(2.0e-12)"
2286	33847_1.R1010	"keyword:transcription(2.0e-12),keyword:myb(2.0e-12)"
2287	jC-atXLIB327402P1h04b1	"keyword:transcription(2.0e-12),keyword:myb(2.0e-12)"
2288	LIB3177-049-P1-K1-C11	keyword:transcription(2.0e-13)
2289	10099_3.R1010	"keyword:transcription(2.0e-13),keyword:myb(2.0e-13)"
2290	66961_1.R1010	"keyword:transcription(2.0e-13),keyword:myb(2.0e-13)"

2291	jC-atXLIB327410P1b07b1	"keyword:transcription(2.0e-13),keyword:myb(2.0e-13)"
2292	jC-atXmonuni25Db04b1	keyword:transcription(2.0e-15)
2293	17017_1.R1010	"keyword:transcription(2.0e-15),keyword:myb(2.0e-15)"
2294	4301_1.R1010	"keyword:transcription(2.0e-15),keyword:myb(2.0e-15)"
2295	jC-atXLIB327410P4a04b1	"keyword:transcription(2.0e-15),keyword:myb(2.0e-15)"
2296	jC-atXLIB327423P4c02b1	"keyword:transcription(2.0e-15),keyword:myb(2.0e-15)"
2297	jC-atXLIB327423P4e02b1	"keyword:transcription(2.0e-15),keyword:myb(2.0e-15)"
2298	jC-atXLIB327437P2b06a2	"keyword:transcription(2.0e-15),keyword:myb(2.0e-15)"
2299	jC-atXP50C179L20T7096d1	"keyword:transcription(2.0e-15),keyword:myb(2.0e-15)"
2300	130123_1.R1010	keyword:transcription(2.0e-18)
2301	78769_2.R1010	keyword:transcription(2.0e-19)
2302	jC-alX25027Q1E1G08a1	keyword:transcription(2.0e-19)
2303	123111_1.R1010	"keyword:transcription(2.0e-19),keyword:myb(2.0e-19)"
2304	1242_5.R1010	keyword:transcription(2.0e-20)
2305	7033_1.R1010	keyword:transcription(2.0e-24)
2306	LIB3176-039-P1-K1-G11	keyword:transcription(2.0e-24)
2307	jC-atXLIB327437P2f03b2	keyword:transcription(2.0e-25)
2308	LIB3176-043-P1-K1-F7	"keyword:transcription(2.0e-25),keyword:myb(2.0e-25)"
2309	ARABL1-042-Q1-E1-C11	keyword:transcription(2.0e-26)
2310	148635_1.R1010	keyword:transcription(2.0e-27)
2311	3707_1.R1010	keyword:transcription(2.0e-27)
2312	23105_1.R1010	keyword:transcription(2.0e-28)
2313	jC-atXP123C119P10T7027a1	keyword:transcription(2.0e-30)
2314	LIB23-048-Q1-E1-B1	keyword:transcription(2.0e-31)
2315	jC-atXP57C191F16T7058a1	keyword:transcription(2.0e-32)
2316	116873_1.R1010	keyword:transcription(2.0e-33)
2317	LIB24-117-Q1-E1-D4	"keyword:transcription(2.0e-34),keyword:helix-loop-helix(2.0e-34)"
2318	jC-atXLIB327410P1h01a1	keyword:transcription(2.0e-35)
2319	1268235	"keyword:transcription(2.0e-36),keyword:bzip(2.0e-36)"
2320	2722407	keyword:transcription(2.0e-37)
2321	199_7.R1010	keyword:transcription(2.0e-38)
2322	jC-atXP100C269G1T7b1	keyword:transcription(2.0e-38)
2323	73529_1.R1010	keyword:transcription(2.0e-40)
2324	14869_1.R1010	keyword:transcription(2.0e-41)
2325	25965_1.R1010	"keyword:transcription(2.0e-41),keyword:myb(2.0e-41),keyword:dna-binding(2.0e-41)"
2326	LIB3168-071-P1-K1-E9	"keyword:transcription(2.0e-42),keyword:myb(2.0e-42)"
2327	2413363	"keyword:transcription(2.0e-

		45),keyword:myb(2.0e-45)"
2328	957838	keyword:transcription(2.0e-48)
2329	1251_3.R1010	keyword:transcription(2.0e-49)
2330	1701_1.R1010	keyword:transcription(2.0e-53)
2331	2886_1.R1010	keyword:transcription(2.0e-53)
2332	484_4.R1010	keyword:transcription(2.0e-57)
2333	2413906	keyword:transcription(2.0e-62)
2334	199_2.R1010	keyword:transcription(2.0e-62)
2335	1702_2.R1010	keyword:transcription(2.0e-71)
2336	21486_1.R1010	keyword:transcription(2.0e-71)
2337	jC-atXP82CG2C1T7d3	keyword.transcription(2.0e-73)
2338	13267_1.R1010	"keyword:transcription(2.0e-98),keyword:myb(2.0e-98)"
2339	jC-atXLIB327415P3f10a1	"keyword:transcription(3.0e-09),keyword:mads(3.0e-09)"
2340	jC-atXP32C147K3T7d2	"keyword:transcription(3.0e-09),keyword:myb(3.0e-09)"
2341	2739586	"keyword:transcription(3.0e-09),keyword:scarecrow(3.0e-09)"
2342	125611_1.R1010	keyword.transcription(3.0e-10)
2343	jC-atXLIB327417P1d12b1	"keyword:transcription(3.0e-11),keyword:myb(3.0e-11)"
2344	jC-atXLIB327421P4b05b1	"keyword:transcription(3.0e-11),keyword:myb(3.0e-11)"
2345	20371_1.R1010	"keyword:transcription(3.0e-12),keyword:mads(3.0e-12)"
2346	jC-atXP121C118B15T7062d1	"keyword:transcription(3.0e-12),keyword:myb(3.0e-12)"
2347	jC-atXLIB327413P3f10b1	"keyword:transcription(3.0e-13),keyword:myb(3.0e-13)"
2348	397313	keyword.transcription(3.0e-14)
2349	90868_1.R1010	"keyword:transcription(3.0e-14),keyword:myb(3.0e-14)"
2350	jC-atXLIB327413P3a02b1	"keyword:transcription(3.0e-14),keyword:myb(3.0e-14)"
2351	jC-atXLIB327437P2c10a2	"keyword:transcription(3.0e-14),keyword:myb(3.0e-14)"
2352	21472_1.R1010	keyword:transcription(3.0e-15)
2353	43837_1.R1010	"keyword:transcription(3.0e-15),keyword:myb(3.0e-15)"
2354	jC-atXLIB327423P3d05b1	"keyword:transcription(3.0e-16),keyword:myb(3.0e-16)"
2355	LIB3176-019-P1-K1-F12	keyword:transcription(3.0e-17)
2356	34038_1.R1010	"keyword:transcription(3.0e-17),keyword:myb(3.0e-17)"
2357	jC-atXLIB327407P1d12b1	"keyword:transcription(3.0e-17),keyword:myb(3.0e-17)"
2358	jC-atXLIB327416P3a11b1	"keyword:transcription(3.0e-17),keyword:myb(3.0e-17)"
2359	120242_2.R1010	keyword:transcription(3.0e-20)
2360	80106_1.R1010	keyword.transcription(3.0e-22)
2361	36515_1.R1010	keyword:transcription(3.0e-27)
2362	87954_2.R1010	keyword:transcription(3.0e-28)
2363	935761	keyword:transcription(3.0e-30)

2364	15807_1.R1010	keyword:transcription(3.0e-30)
2365	773531	"keyword:transcription(3.0e-30),keyword:bzip(3.0e-30)"
2366	LIB25-059-Q1-E1-G12	"keyword:transcription(3.0e-35),keyword:bzip(3.0e-35)"
2367	LIB3234-018-P1-K1-B4	"keyword:transcription(3.0e-35),keyword:myb(3.0e-35)"
2368	120704_1.R1010	keyword:transcription(3.0e-36)
2369	2413827	keyword:transcription(3.0e-37)
2370	7041_1.R1010	"keyword:transcription(3.0e-37),keyword:myb(3.0e-37),keyword:dna-binding(3.0e-37)"
2371	75257_1.R1010	keyword:transcription(3.0e-50)
2372	LIB23-054-Q1-E1-A3	keyword:transcription(3.0e-50)
2373	LIB3234-084-Q1-K1-D1	keyword:transcription(3.0e-63)
2374	31106_1.R1010	"keyword:transcription(3.0e-64),keyword:myb(3.0e-64)"
2375	5130_1.R1010	keyword:transcription(3.0e-65)
2376	74599_1.R1010	keyword:transcription(3.0e-69)
2377	LIB3177-099-P1-K1-G12	"keyword:transcription(3.0e-72),keyword:myb(3.0e-72)"
2378	87285_1.R1010	"keyword:transcription(3.0e-88),keyword:myb(3.0e-88)"
2379	jC-atXLIB327408P3c12b1	"keyword:transcription(4.0e-09),keyword:AGL(4.0e-09)"
2380	jC-atXLIB327424P1d04b2	"keyword:transcription(4.0e-10),keyword:myb(4.0e-10)"
2381	30731_1.R1010	keyword:transcription(4.0e-11)
2382	2757901	keyword:transcription(4.0e-12)
2383	63254_2.R1010	keyword:transcription(4.0e-13)
2384	jC-atXLIB327407P1e12b1	"keyword:transcription(4.0e-13),keyword:myb(4.0e-13)"
2385	jC-atXLIB327407P3h10b1	"keyword:transcription(4.0e-13),keyword:myb(4.0e-13)"
2386	8444_1.R1010	"keyword:transcription(4.0e-15),keyword:bzip(4.0e-15)"
2387	36955_1.R1010	"keyword:transcription(4.0e-15),keyword:myb(4.0e-15)"
2388	8612_1.R1010	"keyword:transcription(4.0e-17),keyword:bzip(4.0e-17)"
2389	LIB3168-051-P1-K1-C7	"keyword:transcription(4.0e-17),keyword:myb(4.0e-17)"
2390	28758_1.R1010	"keyword:transcription(4.0e-17),keyword:zinc-finger(4.0e-17)"
2391	LIB3168-033-P1-K1-C1	keyword:transcription(4.0e-18)
2392	jC-atXLIB327408P3c12a1	"keyword:transcription(4.0e-18),keyword:AGL(4.0e-18)"
2393	123109_1.R1010	"keyword:transcription(4.0e-20),keyword:myb(4.0e-20)"
2394	jC-atXP61C201E9T7d1	keyword:transcription(4.0e-21)
2395	10519_1.R1010	keyword:transcription(4.0e-22)
2396	jC-atXLIB327426P3b06a1	"keyword:transcription(4.0e-

		22),keyword:scarecrow(4.0e-22)"
2397	jC-atXP96C248B18T7b1	"keyword:transcription(4.0e-23),keyword:myb(4.0e-23)"
2398	LIB3234-050-P1-K1-D5	"keyword:transcription(4.0e-30),keyword:myb(4.0e-30)"
2399	jC-atXLIB327432P2b08b2	keyword:transcription(4.0e-35)
2400	958051	keyword:transcription(4.0e-43)
2401	6799_1.R1010	keyword:transcription(4.0e-43)
2402	LIB3177-044-P1-K2-E1	keyword:transcription(4.0e-46)
2403	2413798	keyword:transcription(4.0e-48)
2404	199_3.R1010	keyword:transcription(4.0e-49)
2405	LIB146-010-Q1-E1-A5	keyword:transcription(4.0e-49)
2406	LIB3234-008-P1-K1-E6	keyword:transcription(4.0e-49)
2407	1242_1.R1010	keyword:transcription(4.0e-60)
2408	17214_1.R1010	keyword:transcription(4.0e-63)
2409	116091_1.R1010	keyword:transcription(4.0e-64)
2410	70096_1.R1010	keyword:transcription(4.0e-76)
2411	26493_1.R1010	keyword:transcription(4.0e-79)
2412	jC-atXLIB327413P2h06b1	"keyword:transcription(5.0e-10),keyword:myb(5.0e-10)"
2413	jC-atXLIB327424P3c09b1	"keyword:transcription(5.0e-10),keyword:myb(5.0e-10)"
2414	LIB22-002-Q1-E1-F5	keyword:transcription(5.0e-11)
2415	jC-atX24061Q1E1B04a1	keyword:transcription(5.0e-12)
2416	116174_1.R1010	keyword:transcription(5.0e-13)
2417	LIB3168-094-P1-K1-C1	keyword:transcription(5.0e-13)
2418	jC-atXLIB327407P2c07b1	"keyword:transcription(5.0e-13),keyword:myb(5.0e-13)"
2419	jC-atXLIB327416P1e04b1	"keyword:transcription(5.0e-13),keyword:myb(5.0e-13)"
2420	jC-atXLIB327422P3b10b2	"keyword:transcription(5.0e-13),keyword:myb(5.0e-13)"
2421	jC-atXLIB327423P4f04b1	"keyword:transcription(5.0e-13),keyword:myb(5.0e-13)"
2422	jC-atXLIB327425P3h02b1	"keyword:transcription(5.0e-13),keyword:myb(5.0e-13)"
2423	19437_1.R1010	"keyword:transcription(5.0e-14),keyword:myb(5.0e-14)"
2424	134494_1.R1010	keyword:transcription(5.0e-15)
2425	19158_1.R1010	"keyword:transcription(5.0e-18),keyword:myb(5.0e-18)"
2426	jC-atXLIB327407P2d04b1	"keyword:transcription(5.0e-18),keyword:myb(5.0e-18)"
2427	LIB3168-075-P1-K1-A12	"keyword:transcription(5.0e-21),keyword:myb(5.0e-21)"
2428	935191	keyword:transcription(5.0e-22)
2429	95605_2.R1010	"keyword:transcription(5.0e-31),keyword:helix-loop-helix(5.0e-31)"
2430	12063_1.R1010	keyword:transcription(5.0e-38)
2431	jC-atXLIB327421P1f03a1	"keyword:transcription(5.0e-56),keyword:myb(5.0e-56)"
2432	jC-atXP39C16213T7s1	"keyword:transcription(5.0e-62),keyword:myb(5.0e-62)"

2433	LIB146-013-Q1-E1-C10	keyword:transcription(6.0e-10)
2434	jC-atXLIB327437P2d05a2	"keyword:transcription(6.0e-10),keyword:myb(6.0e-10)"
2435	84570_1.R1010	"keyword:transcription(6.0e-11),keyword:myb(6.0e-11)"
2436	LIB23-007-Q1-E1-D7	keyword:transcription(6.0e-12)
2437	jC-atXP65C209F23T7096d1	"keyword:transcription(6.0e-13),keyword:myb(6.0e-13)"
2438	30826_1.R1010	"keyword:transcription(6.0e-16),keyword:myb(6.0e-16)"
2439	LIB22-035-Q1-E1-E1	keyword:transcription(6.0e-17)
2440	53812_1.R1010	"keyword:transcription(6.0e-18),keyword:bzip(6.0e-18)"
2441	jC-atXLIB327406P3c02b2	"keyword:transcription(6.0e-18),keyword:myb(6.0e-18)"
2442	jC-atXLIB327407P2a01b1	"keyword:transcription(6.0e-18),keyword:myb(6.0e-18)"
2443	102790_1.R1010	"keyword:transcription(6.0e-19),keyword:myb(6.0e-19)"
2444	jC-atXLIB327408P3b01a1	keyword:transcription(6.0e-20)
2445	LIB3176-049-P1-K1-C7	keyword:transcription(6.0e-21)
2446	76_2.R1010	"keyword:transcription(6.0e-21),keyword:dna-binding(6.0e-21)"
2447	8150_1.R1010	keyword:transcription(6.0e-30)
2448	LIB3234-072-P1-K1-H7	keyword:transcription(6.0e-35)
2449	2413368	"keyword:transcription(6.0e-38),keyword:myb(6.0e-38)"
2450	87954_1.R1010	keyword:transcription(6.0e-42)
2451	2413889	keyword:transcription(6.0e-63)
2452	jC-atXLIB327422P3d01b2	keyword:transcription(6.0e-63)
2453	jC-atXLIB327410P1d03b1	"keyword:transcription(7.0e-09),keyword:myb(7.0e-09)"
2454	jC-atXLIB327413P2c03b1	"keyword:transcription(7.0e-09),keyword:myb(7.0e-09)"
2455	2580901	keyword:transcription(7.0e-10)
2456	123071_1.R1010	"keyword:transcription(7.0e-13),keyword:myb(7.0e-13)"
2457	LIB3176-027-P1-K1-F5	"keyword:transcription(7.0e-15),keyword:myb(7.0e-15)"
2458	7041_2.R1010	"keyword:transcription(7.0e-17),keyword:myb(7.0e-17),keyword:dna-binding(7.0e-17)"
2459	LIB3168-070-P1-K1-E7	keyword:transcription(7.0e-23)
2460	1456_3.R1010	keyword:transcription(7.0e-26)
2461	jC-atXP12C103L19T7087a1	keyword:transcription(7.0e-26)
2462	LIB3177-036-P1-K1-B2	keyword:transcription(7.0e-29)
2463	1269428	keyword:transcription(7.0e-38)
2464	88042_1.R1010	keyword:transcription(7.0e-41)
2465	LIB3234-019-P1-K1-E12	keyword:transcription(7.0e-46)
2466	937784	keyword:transcription(7.0e-52)
2467	LIB22-029-Q1-E1-G9	keyword:transcription(7.0e-54)
2468	LIB24-094-Q1-E1-G3	keyword:transcription(7.0e-59)

2469	199_1.R1010	keyword:transcription(7.0e-63)
2470	LIB3175-052-P1-K1-G10	"keyword:transcription(7.0e-64),keyword:bzip(7.0e-64)"
2471	LIB3177-055-P1-K1-C3	keyword:transcription(7.0e-70)
2472	jC-atXLIB327412P1h12b1	"keyword:transcription(8.0e-09),keyword:myb(8.0e-09)"
2473	jC-atXLIB327413P4d02b1	"keyword:transcription(8.0e-09),keyword:myb(8.0e-09)"
2474	LIB3234-084-Q1-K1-A4	keyword:transcription(8.0e-13)
2475	129437_1.R1010	"keyword:transcription(8.0e-13),keyword:myb(8.0e-13)"
2476	jC-atXLIB327415P3b09b1	"keyword:transcription(8.0e-15),keyword:myb(8.0e-15)"
2477	125840_1.R1010	"keyword:transcription(8.0e-16),keyword:myb(8.0e-16)"
2478	5416_3.R1010	keyword:transcription(8.0e-20)
2479	2869_1.R1010	"keyword:transcription(8.0e-22),keyword:myb(8.0e-22),keyword:dna-binding(8.0e-22)"
2480	LIB3234-038-P1-K1-H9	keyword:transcription(8.0e-28)
2481	1053361	keyword:transcription(8.0e-30)
2482	LIB3176-028-P1-K1-H11	keyword:transcription(8.0e-36)
2483	LIB25-027-Q1-E1-H2	keyword:transcription(8.0e-46)
2484	34883_1.R1010	keyword:transcription(8.0e-56)
2485	8486_1.R1010	keyword:transcription(8.0e-59)
2486	jC-atXLIB327408P4h04b1	"keyword:transcription(8.0e-71),keyword:myb(8.0e-71)"
2487	jC-atXP12C103L24T7091a1	keyword:transcription(9.0e-09)
2488	26106_1.R1010	"keyword:transcription(9.0e-12),keyword:myb(9.0e-12)"
2489	jC-atXP118C144J15T7093d2	"keyword:transcription(9.0e-13),keyword:myb(9.0e-13)"
2490	jC-atXLIB327413P3e08b1	"keyword:transcription(9.0e-15),keyword:myb(9.0e-15)"
2491	jC-atXLIB327424P1f01b2	"keyword:transcription(9.0e-15),keyword:myb(9.0e-15)"
2492	jC-atXmonuni26Ad12a1	keyword:transcription(9.0e-40)
2493	1702_1.R1010	keyword:transcription(9.0e-51)
2494	906440	keyword:transcription(9.0e-63)
2495	17656_1.R1010	keyword:zinc-finger(0.0e+00)
2496	LIB3234-080-P1-K1-G6	keyword:zinc-finger(0.0e+00)
2497	2446113	keyword:zinc-finger(1.0e-09)
2498	142749_1.R1010	keyword:zinc-finger(1.0e-09)
2499	LIB3175-061-P1-K1-D9	keyword:zinc-finger(1.0e-09)
2500	LIB3234-095-P1-K1-H11	keyword:zinc-finger(1.0e-11)
2501	9370_1.R1010	keyword:zinc-finger(1.0e-114)
2502	973_1.R1010	keyword:zinc-finger(1.0e-116)
2503	9986_1.R1010	keyword:zinc-finger(1.0e-118)
2504	LIB146-012-Q1-E1-G4	keyword:zinc-finger(1.0e-12)
2505	LIB3175-016-P1-K1-G5	keyword:zinc-finger(1.0e-121)
2506	1159660	keyword:zinc-finger(1.0e-133)
2507	930572	keyword:zinc-finger(1.0e-14)
2508	9370_2.R1010	keyword:zinc-finger(1.0e-14)

2509	7360_1.R1010	keyword:zinc-finger(1.0e-15)
2510	LIB22-013-Q1-E1-D12	keyword:zinc-finger(1.0e-15)
2511	jC-atXP94CH5G8T7b1	keyword:zinc-finger(1.0e-152)
2512	LIB3177-079-P1-K1-E4	keyword:zinc-finger(1.0e-16)
2513	2094_1.R1010	keyword:zinc-finger(1.0e-169)
2514	69843_2.R1010	keyword:zinc-finger(1.0e-18)
2515	2756827	keyword:zinc-finger(1.0e-23)
2516	jC-atXLIB327413P4g05a1	keyword:zinc-finger(1.0e-23)
2517	2757000	keyword:zinc-finger(1.0e-24)
2518	25151_1.R1010	keyword:zinc-finger(1.0e-24)
2519	jC-atXP115C250H2T7d1	keyword:zinc-finger(1.0e-29)
2520	LIB23-036-Q1-E1-E9	keyword:zinc-finger(1.0e-40)
2521	4802_1.R1010	keyword:zinc-finger(1.0e-42)
2522	jC-atXP33C148C13T7s2	"keyword:zinc-finger(1.0e-44),keyword:zinc-finger(1.0e-44)"
2523	jC-atXP69C219E3T7061a1	keyword:zinc-finger(1.0e-49)
2524	LIB3234-085-Q1-K1-B8	keyword:zinc-finger(1.0e-64)
2525	24421_1.R1010	keyword:zinc-finger(1.0e-70)
2526	2596365	keyword:zinc-finger(2.0e-09)
2527	57820_2.R1010	keyword:zinc-finger(2.0e-11)
2528	LIB22-021-Q1-E1-G10	keyword:zinc-finger(2.0e-12)
2529	933630	keyword:zinc-finger(2.0e-14)
2530	LIB3234-083-Q1-K1-E7	keyword:zinc-finger(2.0e-14)
2531	jC-atXLIB327426P2d01b1	keyword:zinc-finger(2.0e-15)
2532	104719_1.R1010	keyword:zinc-finger(2.0e-18)
2533	LIB3234-096-P1-K1-G6	keyword:zinc-finger(2.0e-19)
2534	11941_1.R1010	keyword:zinc-finger(2.0e-22)
2535	LIB23-054-Q1-E1-F11	keyword:zinc-finger(2.0e-26)
2536	2393482	"keyword:zinc-finger(2.0e-27),keyword:zinc-finger(2.0e-27)"
2537	397327	keyword:zinc-finger(2.0e-34)
2538	2805_1.R1010	keyword:zinc-finger(2.0e-42)
2539	937609	keyword:zinc-finger(2.0e-47)
2540	5216_1.R1010	keyword:zinc-finger(2.0e-47)
2541	jC-atXLIB327437P2f01b2	keyword:zinc-finger(2.0e-49)
2542	2094_3.R1010	keyword:zinc-finger(2.0e-51)
2543	58023_1.R1010	keyword:zinc-finger(2.0e-54)
2544	jC-atXP118C142N22T7035a1	keyword:zinc-finger(2.0e-56)
2545	LIB3234-043-P1-K1-H4	keyword:zinc-finger(2.0e-62)
2546	12614_1.R1010	keyword:zinc-finger(2.0e-64)
2547	48833_1.R1010	keyword:zinc-finger(2.0e-75)
2548	13769_1.R1010	"keyword:zinc-finger(2.0e-88),keyword:zinc-finger(2.0e-88)"
2549	2112_1.R1010	keyword:zinc-finger(2.0e-95)
2550	jC-atXP69C218L15T7058a1	keyword:zinc-finger(3.0e-09)
2551	LIB3168-084-P1-K1-C4	keyword:zinc-finger(3.0e-10)
2552	2757920	keyword:zinc-finger(3.0e-13)
2553	LIB3177-044-P1-K2-A7	keyword:zinc-finger(3.0e-14)
2554	1520759	keyword:zinc-finger(3.0e-15)
2555	15938_1.R1010	keyword:zinc-finger(3.0e-19)
2556	34424_1.R1010	keyword:zinc-finger(3.0e-19)

2557	jC-atXLIB327407P1c04a1	keyword:zinc-finger(3.0e-20)
2558	LIB3234-026-Q1-K1-F7	keyword:zinc-finger(3.0e-21)
2559	2759682	keyword:zinc-finger(3.0e-26)
2560	LIB22-066-Q1-E1-G9	keyword:zinc-finger(3.0e-30)
2561	jC-atXLIB327417P1h12a1	keyword:zinc-finger(3.0e-31)
2562	jC-atXP69C219D5T7029a1	keyword:zinc-finger(3.0e-31)
2563	38176_1.R1010	keyword:zinc-finger(3.0e-38)
2564	15536_1.R1010	keyword:zinc-finger(3.0e-39)
2565	69843_1.R1010	keyword:zinc-finger(3.0e-40)
2566	LIB3177-044-P1-K2-B7	keyword:zinc-finger(3.0e-40)
2567	LIB24-078-Q1-E1-H8	keyword:zinc-finger(3.0e-41)
2568	101306_1.R1010	keyword:zinc-finger(3.0e-43)
2569	4552_1.R1010	keyword:zinc-finger(3.0e-47)
2570	6617_1.R1010	keyword:zinc-finger(3.0e-49)
2571	2112_3.R1010	keyword:zinc-finger(3.0e-51)
2572	LIB23-031-Q1-E1-E10	keyword:zinc-finger(3.0e-55)
2573	LIB3234-010-P1-K1-B9	keyword:zinc-finger(3.0e-60)
2574	jC-atXLIB327431P2d03a1	keyword:zinc-finger(4.0e-16)
2575	2764378	keyword:zinc-finger(4.0e-17)
2576	jC-atXLIB327413P4e09b1	keyword:zinc-finger(4.0e-17)
2577	LIB24-085-Q1-E1-E9	keyword:zinc-finger(4.0e-19)
2578	8143_1.R1010	keyword:zinc-finger(4.0e-20)
2579	506548	keyword:zinc-finger(4.0e-22)
2580	13864_2.R1010	keyword:zinc-finger(4.0e-23)
2581	jC-atXP3C81A7T7020a1	keyword:zinc-finger(4.0e-23)
2582	63653_2.R1010	keyword:zinc-finger(4.0e-25)
2583	33551_1.R1010	keyword:zinc-finger(4.0e-33)
2584	48092_1.R1010	keyword:zinc-finger(4.0e-34)
2585	jC-atXLIB327426P1d11b1	keyword:zinc-finger(4.0e-36)
2586	10012_1.R1010	keyword:zinc-finger(4.0e-37)
2587	LIB35-054-Q1-E1-B3	keyword:zinc-finger(4.0e-44)
2588	jC-alXLIB327435P3e07b1	keyword:zinc-finger(4.0e-83)
2589	2750080	keyword:zinc-finger(5.0e-13)
2590	ARABL1-038-Q1-B1-G10	keyword:zinc-finger(5.0e-13)
2591	2596322	keyword:zinc-finger(5.0e-19)
2592	LIB3177-016-P1-K1-G2	keyword:zinc-finger(5.0e-20)
2593	119921_1.R1010	keyword:zinc-finger(5.0e-32)
2594	29459_1.R1010	keyword:zinc-finger(5.0e-35)
2595	83449_1.R1010	keyword:zinc-finger(5.0e-38)
2596	101306_2.R1010	keyword:zinc-finger(5.0e-41)
2597	jC-atXLIB327410P3b02a1	keyword:zinc-finger(5.0e-50)
2598	9815_1.R1010	keyword:zinc-finger(5.0e-53)
2599	LIB25-047-Q1-E1-C1	keyword:zinc-finger(6.0e-13)
2600	LIB3234-057-P1-K1-C9	keyword:zinc-finger(6.0e-14)
2601	LIB3175-052-P1-K1-H11	keyword:zinc-finger(6.0e-21)
2602	2112_7.R1010	keyword:zinc-finger(6.0e-25)
2603	LIB3177-010-P1-K1-A11	keyword:zinc-finger(6.0e-33)
2604	jC-atXP87C244H16T7b1	keyword:zinc-finger(6.0e-54)
2605	jC-atX25060Q1E1G04a1	keyword:zinc-finger(6.0e-73)
2606	1053262	keyword:zinc-finger(6.0e-86)
2607	18064_1.R1010	"keyword:zinc-finger(6.0e-98),keyword:zinc-finger(6.0e-98)"
2608	6226_1.R1010	keyword:zinc-finger(7.0e-21)

2609	1932866	keyword:zinc-finger(7.0e-24)
2610	906994	keyword:zinc-finger(7.0e-37)
2611	76960_1.R1010	keyword:zinc-finger(7.0e-60)
2612	LIB3177-093-P1-K1-A11	keyword:zinc-finger(7.0e-65)
2613	LIB3177-019-P1-K1-E5	keyword:zinc-finger(8.0e-09)
2614	jC-atX22051Q1E1D08b1	keyword:zinc-finger(8.0e-11)
2615	LIB3168-004-P1-K1-F7	keyword:zinc-finger(8.0e-15)
2616	LIB3176-094-P1-K1-G3	keyword:zinc-finger(8.0e-16)
2617	115674_1.R1010	keyword:zinc-finger(8.0e-31)
2618	397182	keyword:zinc-finger(8.0e-42)
2619	LIB3168-044-P1-K1-C2	keyword:zinc-finger(8.0e-59)
2620	45108_1.R1010	keyword:zinc-finger(9.0e-10)
2621	LIB3176-051-P1-K1-E2	keyword:zinc-finger(9.0e-15)
2622	jC-atXLIB327426P1d11a1	keyword:zinc-finger(9.0e-17)
2623	2062896	keyword:zinc-finger(9.0e-34)
2624	LIB23-054-Q1-E1-F5	keyword:zinc-finger(9.0e-35)
2625	LIB25-033-Q1-E1-H4	keyword:zinc-finger(9.0e-45)
2626	122787_1.R1010	keyword:zinc-finger(9.0e-69)
2627	97662_1.R1010	lim(HMM:0.0017)
2628	1167_2.R1010	lim(HMM:0.063)
2629	32106_1.R1010	lim(HMM:0.092)
2630	13793_1.R1010	lim(HMM:1.5e-33)
2631	32106_2.R1010	lim(HMM:1.7e-16)
2632	50585_1.R1010	lim(HMM:1.8e-16)
2633	LIB3176-036-P1-K1-E4	lim(HMM:2.2e-10)
2634	1167_3.R1010	lim(HMM:2.5e-15)
2635	19353_2.R1010	lim(HMM:3.3e-14)
2636	LIB22-059-Q1-E1-H4	lim(HMM:3.4)
2637	6243_1.R1010	lim(HMM:4.1e-35)
2638	1167_1.R1010	lim(HMM:8.3e-35)
2639	2763256	linker_histone(HMM:0.00034)
2640	LIB3176-036-P1-K1-H7	linker_histone(HMM:0.00078)
2641	11718_17.R1010	linker_histone(HMM:0.006)
2642	697_2.R1010	linker_histone(HMM:0.01)
2643	17727_3.R1010	linker_histone(HMM:1.6e-06)
2644	935999	linker_histone(HMM:1.6e-28)
2645	17727_2.R1010	linker_histone(HMM:1.8e-10)
2646	4256_1.R1010	linker_histone(HMM:3.3e-22)
2647	67_1.R1010	linker_histone(HMM:3.3e-37)
2648	127_1.R1010	linker_histone(HMM:3e-22)
2649	697_1.R1010	linker_histone(HMM:4e-35)
2650	jC-atXLIB327426P2e12b1	linker_histone(HMM:5.5e-24)
2651	jC-atXP79C238C1T7d2	linker_histone(HMM:6.3e-15)
2652	128_1.R1010	linker_histone(HMM:7.8e-29)
2653	128_3.R1010	linker_histone(HMM:7.8e-29)
2654	398632	myb_dna-binding(HMM:0.00026)
2655	19696_1.R1010	myb_dna-binding(HMM:0.00029)
2656	LIB23-041-Q1-E1-G1	myb_dna-binding(HMM:0.00031)
2657	51036_2.R1010	myb_dna-binding(HMM:0.00038)
2658	LIB3175-043-P1-K1-A3	myb_dna-

		binding(HMM:0.00042)
2659	6718_1.R1010	myb_dna-binding(HMM:0.00053)
2660	29160_1.R1010	myb_dna-binding(HMM:0.00094)
2661	LIB23-003-Q1-E1-C10	myb_dna-binding(HMM:0.0012)
2662	22627_1.R1010	myb_dna-binding(HMM:0.0013)
2663	16833	myb_dna-binding(HMM:0.0015)
2664	118469_1.R1010	myb_dna-binding(HMM:0.0021)
2665	2764125	myb_dna-binding(HMM:0.0025)
2666	19235_1.R1010	myb_dna-binding(HMM:0.0028)
2667	LIB3168-051-P1-K1-E4	myb_dna-binding(HMM:0.0082)
2668	116942_1.R1010	myb_dna-binding(HMM:0.027)
2669	LIB3175-034-P1-K1-A12	myb_dna-binding(HMM:0.054)
2670	59403_2.R1010	myb_dna-binding(HMM:0.063)
2671	70528_1.R1010	myb_dna-binding(HMM:0.14)
2672	LIB146-030-Q1-K1-B6	myb_dna-binding(HMM:0.14)
2673	906292	myb_dna-binding(HMM:0.65)
2674	338_2.R1010	myb_dna-binding(HMM:0.85)
2675	2748969	myb_dna-binding(HMM:0.87)
2676	PLN_g1495252	myb_dna-binding(HMM:1.1e-46)
2677	LIB23-037-Q1-E1-H11	myb_dna-binding(HMM:1.2e-18)
2678	PLN_g455462	myb_dna-binding(HMM:1.2e-39)
2679	PLN_g217858	myb_dna-binding(HMM:1.2e-41)
2680	PLN_g1254994	myb_dna-binding(HMM:1.3e-41)
2681	21100_1.R1010	myb_dna-binding(HMM:1.3e-42)
2682	337_1.R1010	myb_dna-binding(HMM:1.3e-44)
2683	339_1.R1010	myb_dna-binding(HMM:1.3e-44)
2684	LIB3168-071-P1-K1-C6	myb_dna-binding(HMM:1.4e-09)
2685	117448_1.R1010	myb_dna-binding(HMM:1.4e-17)
2686	22848_1.R1010	myb_dna-binding(HMM:1.4e-18)
2687	7193_1.R1010	myb_dna-binding(HMM:1.5)
2688	1751_1.R1010	myb_dna-binding(HMM:1.5e-37)
2689	96_1.R1010	myb_dna-binding(HMM:1.5e-44)
2690	338_1.R1010	myb_dna-binding(HMM:1.5e-45)
2691	PLN_g3941471	myb_dna-binding(HMM:1.6e-38)
2692	125583_2.R1010	myb_dna-binding(HMM:1.7)
2693	jC-atXN563193a2	myb_dna-binding(HMM:1.7)
2694	117090_1.R1010	myb_dna-binding(HMM:1.8e-17)
2695	1749_1.R1010	myb_dna-binding(HMM:1.8e-35)
2696	33812_1.R1010	myb_dna-binding(HMM:1.8e-37)
2697	21524_1.R1010	myb_dna-binding(HMM:1.9e-30)
2698	1740_1.R1010	myb_dna-binding(HMM:1.9e-40)
2699	LIB22-001-Q1-E1-G3	myb_dna-binding(HMM:2.1e-06)
2700	10288_1.R1010	myb_dna-binding(HMM:2.1e-11)
2701	1748_1.R1010	myb_dna-binding(HMM:2.2e-43)
2702	368_1.R1010	myb_dna-binding(HMM:2.2e-43)
2703	25441_1.R1010	myb_dna-binding(HMM:2.2e-45)
2704	PLN_g1263092	myb_dna-binding(HMM:2.2e-45)
2705	2763242	myb_dna-binding(HMM:2.3e-16)
2706	PLN_g3941435	myb_dna-binding(HMM:2.3e-39)
2707	1753_1.R1010	myb_dna-binding(HMM:2.4e-44)
2708	6889_1.R1010	myb_dna-binding(HMM:2.5e-09)
2709	494_1.R1010	myb_dna-binding(HMM:2.5e-11)

2710	1747_2.R1010	myb_dna-binding(HMM:2.5e-15)
2711	PLN_g1732512	myb_dna-binding(HMM:2.5e-42)
2712	1752_1.R1010	myb_dna-binding(HMM:2.5e-45)
2713	1750_1.R1010	myb_dna-binding(HMM:2.6e-38)
2714	1744_1.R1010	myb_dna-binding(HMM:2.6e-41)
2715	8478_1.R1010	myb_dna-binding(HMM:2.7e-09)
2716	17177_1.R1010	myb_dna-binding(HMM:2.7e-31)
2717	LIB3177-091-P1-K1-F4	myb_dna-binding(HMM:2.9e-26)
2718	LIB3177-078-P1-K1-F8	myb_dna-binding(HMM:2.9e-32)
2719	19235_2.R1010	myb_dna-binding(HMM:2e-05)
2720	367_2.R1010	myb_dna-binding(HMM:3.1e-05)
2721	PLN_g2280527	myb_dna-binding(HMM:3.2e-42)
2722	725_1.R1010	myb_dna-binding(HMM:3.2e-44)
2723	7193_2.R1010	myb_dna-binding(HMM:3.4e-43)
2724	1033_1.R1010	myb_dna-binding(HMM:3.7e-41)
2725	1338_1.R1010	myb_dna-binding(HMM:3.8e-11)
2726	LIB24-006-Q1-E1-A2	myb_dna-binding(HMM:3.8e-21)
2727	1023_1.R1010	myb_dna-binding(HMM:4.3e-44)
2728	1737_1.R1010	myb_dna-binding(HMM:4.8e-47)
2729	1743_1.R1010	myb_dna-binding(HMM:4.9e-36)
2730	PLN_g3941467	myb_dna-binding(HMM:5.1e-36)
2731	1333_1.R1010	myb_dna-binding(HMM:5.1e-46)
2732	1738_1.R1010	myb_dna-binding(HMM:5.1e-46)
2733	9038_1.R1010	myb_dna-binding(HMM:5.3e-12)
2734	1034_1.R1010	myb_dna-binding(HMM:5.4e-16)
2735	225_1.R1010	myb_dna-binding(HMM:5.6e-42)
2736	1486_1.R1010	myb_dna-binding(HMM:5.8e-31)
2737	936051	myb_dna-binding(HMM:5.9e-14)
2738	PLN_g2832407	myb_dna-binding(HMM:6.1e-35)
2739	1032_1.R1010	myb_dna-binding(HMM:6.3e-42)
2740	PLN_g2346965	myb_dna-binding(HMM:6e-05)
2741	LIB3175-046-P1-K1-B10	myb_dna-binding(HMM:6e-22)
2742	2757484	myb_dna-binding(HMM:7.1e-18)
2743	1772_2.R1010	myb_dna-binding(HMM:7.1e-47)
2744	1738_2.R1010	myb_dna-binding(HMM:7.6e-34)
2745	10057_1.R1010	myb_dna-binding(HMM:7e-10)
2746	8189_1.R1010	myb_dna-binding(HMM:7e-20)
2747	43001_1.R1010	myb_dna-binding(HMM:8.3e-10)
2748	10057_3.R1010	myb_dna-binding(HMM:8.6e-10)
2749	335_1.R1010	myb_dna-binding(HMM:8.8e-42)
2750	1747_1.R1010	myb_dna-binding(HMM:8.9e-42)
2751	1739_1.R1010	myb_dna-binding(HMM:9.5e-44)
2752	1750_2.R1010	myb_dna-binding(HMM:9.6e-08)
2753	LIB3175-061-P1-K1-F8	nam(HMM:0.0021)
2754	jC-atXLIB327424P1g06b2	nam(HMM:0.0048)
2755	398614	nam(HMM:0.04)
2756	28582_1.R1010	nam(HMM:0.2)
2757	jC-atXLIB327430P1e05b1	nam(HMM:0.37)
2758	LIB3175-076-P1-K1-B2	nam(HMM:0.88)
2759	623015	nam(HMM:1.1e-05)
2760	12650_4.R1010	nam(HMM:1.1e-07)
2761	2596320	nam(HMM:1.1e-15)
2762	8647_2.R1010	nam(HMM:1.1e-35)
2763	6414_1.R1010	nam(HMM:1.1e-78)

2764	LIB3234-050-P1-K1-F8	nam(HMM:1.2e-09)
2765	LIB3234-059-P1-K1-G11	nam(HMM:1.2e-22)
2766	958017	nam(HMM:1.2e-26)
2767	71466_1.R1010	nam(HMM:1.3e-17)
2768	933621	nam(HMM:1.3e-26)
2769	6010_1.R1010	nam(HMM:1.3e-80)
2770	76966_2.R1010	nam(HMM:1.4e-20)
2771	120288_1.R1010	nam(HMM:1.4e-78)
2772	LIB22-002-Q1-E1-D6	nam(HMM:1.5e-21)
2773	7903_1.R1010	nam(HMM:1.5e-36)
2774	LIB35-056-Q1-E2-B9	nam(HMM:1.5e-47)
2775	870872	nam(HMM:1.6e-49)
2776	4493_1.R1010	nam(HMM:1.6e-57)
2777	16313_1.R1010	nam(HMM:1.7e-05)
2778	455_1.R1010	nam(HMM:1.7e-82)
2779	2758682	nam(HMM:1.8e-34)
2780	28833_1.R1010	nam(HMM:1.9e-82)
2781	LIB3176-085-P1-K1-E10	nam(HMM:2.1e-10)
2782	LIB23-062-Q1-E1-C10	nam(HMM:2.1e-23)
2783	12650_1.R1010	nam(HMM:2.1e-79)
2784	LIB3168-082-P1-K1-A8	nam(HMM:2.3e-81)
2785	ARABL1-033-Q1-B1-G2	nam(HMM:2.4e-58)
2786	LIB23-027-Q1-E1-F3	nam(HMM:2.5e-05)
2787	LIB24-107-Q1-E1-D7	nam(HMM:2.6e-07)
2788	4281_2.R1010	nam(HMM:2.6e-10)
2789	135_1.R1010	nam(HMM:2.6e-91)
2790	54574_1.R1010	nam(HMM:2.7e-81)
2791	LIB23-066-Q1-E1-B1	nam(HMM:2.8e-33)
2792	957497	nam(HMM:2.8e-59)
2793	23543_1.R1010	nam(HMM:2e-12)
2794	521_1.R1010	nam(HMM:2e-85)
2795	17791_1.R1010	nam(HMM:3.1e-63)
2796	3089_1.R1010	nam(HMM:3.1e-89)
2797	24699_1.R1010	nam(HMM:3.4e-16)
2798	19379_1.R1010	nam(HMM:3.6e-50)
2799	1033258	nam(HMM:3e-07)
2800	30659_1.R1010	nam(HMM:4.1e-10)
2801	jC-atXP123C117E1T7036d1	nam(HMM:4.2e-13)
2802	12539_1.R1010	nam(HMM:4.4e-26)
2803	2762247	nam(HMM:4.5e-07)
2804	jC-atXLIB327408P1d11b1	nam(HMM:4.5e-59)
2805	200_1.R1010	nam(HMM:4.5e-90)
2806	ARABL1-045-Q1-B1-E8	nam(HMM:4.7e-26)
2807	LIB3175-027-P1-K1-B12	nam(HMM:4.9e-29)
2808	76966_1.R1010	nam(HMM:5.2e-09)
2809	12365_1.R1010	nam(HMM:5.2e-22)
2810	4281_1.R1010	nam(HMM:5.7e-40)
2811	17124_1.R1010	nam(HMM:5e-58)
2812	273_1.R1010	nam(HMM:6.1e-91)
2813	5370_1.R1010	nam(HMM:6.2e-16)
2814	LIB35-028-Q1-E1-B12	nam(HMM:6.7e-06)
2815	29965_1.R1010	nam(HMM:6.7e-59)
2816	LIB3168-083-P1-K1-F5	nam(HMM:6.9e-06)
2817	34649_1.R1010	nam(HMM:7.3e-10)

2818	12405_1.R1010	nam(HMM:7.5e-10)
2819	LIB24-045-Q1-E1-H6	nam(HMM:7.7e-29)
2820	jC-atXLIB327424P3f06b1	nam(HMM:7.8)
2821	33543_1.R1010	nam(HMM:7e-84)
2822	LIB3176-106-P1-K1-E2	nam(HMM:8.3e-10)
2823	LIB22-002-Q1-E1-E9	nam(HMM:8.7e-11)
2824	18292_1.R1010	nam(HMM:8.8e-86)
2825	2047367	nam(HMM:9.2e-64)
2826	8647_1.R1010	nam(HMM:9.4e-38)
2827	LIB3177-007-P1-K1-E7	nap_family(HMM:0.0014)
2828	30951_1.R1010	nap_family(HMM:0.0067)
2829	906184	nap_family(HMM:0.023)
2830	LIB3176-036-P1-K1-A6	nap_family(HMM:0.065)
2831	jC-atXP62C203C3T7022a1	nap_family(HMM:1.1e-05)
2832	LIB3177-005-P1-K1-B6	nap_family(HMM:1.4e-05)
2833	LIB3175-004-P1-K1-E9	nap_family(HMM:2.6e-06)
2834	2852_1.R1010	nap_family(HMM:2.7e-09)
2835	4462_1.R1010	nap_family(HMM:3.1e-13)
2836	2798_1.R1010	nap_family(HMM:3e-07)
2837	3157_1.R1010	nap_family(HMM:4.3e-08)
2838	8405_1.R1010	nap_family(HMM:4.4e-09)
2839	jC-atX22045Q1E1C02b1	nap_family(HMM:5.3e-15)
2840	21195_1.R1010	nap_family(HMM:5.6e-37)
2841	LIB3177-021-P1-K2-A7	nap_family(HMM:5.8e-16)
2842	2852_2.R1010	nap_family(HMM:7.9e-103)
2843	LIB3168-067-P1-K1-F5	phd(HMM:0.013)
2844	1620_1.R1010	phd(HMM:0.015)
2845	57640_1.R1010	phd(HMM:0.02)
2846	1619_1.R1010	phd(HMM:0.1)
2847	129014_1.R1010	phd(HMM:0.34)
2848	LIB3234-096-P1-K1-C2	phd(HMM:0.47)
2849	LIB23-021-Q2-E1-C12	phd(HMM:1.1e-06)
2850	95652_1.R1010	phd(HMM:1.5e-08)
2851	LIB22-063-Q1-E1-C9	phd(HMM:1.6e-12)
2852	LIB3168-006-P1-K1-E7	phd(HMM:2e-15)
2853	jC-atXL1044Q1E1G11a1	phd(HMM:3.4e-13)
2854	jC-atXP60C197M21T7027a1	phd(HMM:3.5e-09)
2855	LIB3177-015-P1-K2-B1	phd(HMM:3.7e-05)
2856	157847_1.R1010	phd(HMM:5.8e-09)
2857	103629_1.R1010	phd(HMM:7.5e-08)
2858	2538_1.R1010	phd(HMM:7e-12)
2859	2538_3.R1010	phd(HMM:7e-12)
2860	jC-atXP44C171F7T7024a1	phd(HMM:7e-12)
2861	LIB23-031-Q1-E1-G5	phd(HMM:9e-05)
2862	LIB3175-033-P1-K1-E1	response_reg(HMM:0.00012)
2863	LIB3177-016-P1-K1-C5	response_reg(HMM:0.00074)
2864	LIB3177-020-P1-K1-E2	response_reg(HMM:1.2)
2865	LIB3176-028-P1-K1-A2	response_reg(HMM:1.2e-13)
2866	244_1.R1010	response_reg(HMM:1.2e-23)
2867	393_1.R1010	response_reg(HMM:1.3e-26)
2868	2413769	response_reg(HMM:1.5e-06)
2869	403_2.R1010	response_reg(HMM:1.5e-28)
2870	1327644	response_reg(HMM:1.7e-09)
2871	2748920	response_reg(HMM:1.8e-16)

2872	395_1.R1010	response_reg(HMM:1.8e-27)
2873	7957_1.R1010	response_reg(HMM:1.8e-27)
2874	21872_1.R1010	response_reg(HMM:3.1e-32)
2875	403_1.R1010	response_reg(HMM:3.5e-29)
2876	21672_1.R1010	response_reg(HMM:3.8e-06)
2877	PLN_g3953604	response_reg(HMM:3e-10)
2878	PLN_g1679802	response_reg(HMM:4.1e-28)
2879	256_1.R1010	response_reg(HMM:4.4e-26)
2880	262_1.R1010	response_reg(HMM:4.4e-32)
2881	PLN_g3953594	response_reg(HMM:4.7e-26)
2882	LIB3175-052-P1-K1-F4	response_reg(HMM:5e-32)
2883	jC-atXP96CH2D6T7b1	response_reg(HMM:6.1e-27)
2884	391_1.R1010	response_reg(HMM:8.2e-27)
2885	jC-atXP29C138J22T7047d1	response_reg(HMM:8.8e-21)
2886	8195_1.R1010	sbpb(HMM:0.0021)
2887	22477_2.R1010	sbpb(HMM:0.0031)
2888	735947	sbpb(HMM:0.22)
2889	22477_1.R1010	sbpb(HMM:1.2e-42)
2890	19483_1.R1010	sbpb(HMM:1.4e-13)
2891	6824_1.R1010	sbpb(HMM:4.5e-45)
2892	1224_1.R1010	sbpb(HMM:4.8e-46)
2893	LIB22-030-Q1-E1-F1	sbpb(HMM:7.4e-46)
2894	394856	sbpb(HMM:8e-07)
2895	1158768	sbpb(HMM:9.5e-45)
2896	LIB3176-024-P1-K1-G3	scr(HMM:0.00023)
2897	10912_3.R1010	scr(HMM:0.0014)
2898	LIB3168-058-P1-K1-F3	scr(HMM:0.0031)
2899	68978_1.R1010	scr(HMM:0.01)
2900	jC-atXN38694a1	scr(HMM:0.03)
2901	57113_1.R1010	scr(HMM:1)
2902	99356_1.R1010	scr(HMM:1.1e-06)
2903	81940_1.R1010	scr(HMM:1.1e-14)
2904	34737_1.R1010	scr(HMM:1.2e-17)
2905	115765_1.R1010	scr(HMM:1.3e-05)
2906	11140_1.R1010	scr(HMM:1.3e-09)
2907	jC-atXLIB327416P2g07a1	scr(HMM:1.4e-09)
2908	LIB22-025-Q1-E1-A1	scr(HMM:1.4e-23)
2909	139933_1.R1010	scr(HMM:1.4e-31)
2910	jC-atXLIB327419P1g05a2	scr(HMM:1.5e-06)
2911	6888_1.R1010	scr(HMM:1.6e-09)
2912	1156_1.R1010	scr(HMM:1.7e-185)
2913	222_1.R1010	scr(HMM:1.8e-185)
2914	LIB3177-036-P1-K1-E3	scr(HMM:1.9e-05)
2915	1155_2.R1010	scr(HMM:1.9e-18)
2916	111122_1.R1010	scr(HMM:2.5e-12)
2917	6443_2.R1010	scr(HMM:2.8e-118)
2918	24475_1.R1010	scr(HMM:2e-09)
2919	5003_1.R1010	scr(HMM:2e-15)
2920	jC-atXLIB327434P1g12b1	scr(HMM:2e-40)
2921	115767_2.R1010	scr(HMM:3.1e-08)
2922	jC-atXLIB327408P2a09a1	scr(HMM:3.3e-05)
2923	36525_1.R1010	scr(HMM:3e-08)
2924	LIB3168-028-P1-K1-B4	scr(HMM:4.2e-05)
2925	586965	scr(HMM:4.2e-12)

2926	19298_1.R1010	scr(HMM:4.5e-11)
2927	51773_1.R1010	scr(HMM:4.6e-05)
2928	LIB24-005-Q1-E1-G12	scr(HMM:5.4e-09)
2929	33892_1.R1010	scr(HMM:5.6e-06)
2930	6443_1.R1010	scr(HMM:6.3e-06)
2931	59776_1.R1010	scr(HMM:7.1e-07)
2932	39_1.R1010	scr(HMM:7.4e-171)
2933	87448_1.R1010	scr(HMM:7.6e-15)
2934	jC-atX22069Q1E1B01a1	scr(HMM:7.8e-36)
2935	88702_1.R1010	scr(HMM:8.3e-29)
2936	1155_1.R1010	scr(HMM:9.2e-188)
2937	LIB3177-080-P1-K1-G7	set(HMM:0.0021)
2938	16791	set(HMM:0.0036)
2939	jC-atXP32C147O24T7d2	set(HMM:0.0065)
2940	119988_1.R1010	set(HMM:1e-23)
2941	20908_1.R1010	set(HMM:2.6e-45)
2942	PLN_g3089624	set(HMM:4.1e-55)
2943	1852_1.R1010	set(HMM:4.9e-56)
2944	590_1.R1010	set(HMM:5.4e-57)
2945	5387_1.R1010	set(HMM:7.1e-08)
2946	LIB3234-004-P1-K1-F1	set(HMM:9.1e-07)
2947	1932_1.R1010	snf2_n(HMM:0.1)
2948	LIB22-063-Q1-E1-C6	snf2_n(HMM:0.13)
2949	7289_1.R1010	snf2_n(HMM:0.2)
2950	3933_1.R1010	snf2_n(HMM:0.97)
2951	117341_1.R1010	snf2_n(HMM:1.1e-08)
2952	1328354	snf2_n(HMM:1.6e-12)
2953	LIB24-048-Q1-E1-G10	snf2_n(HMM:1e-16)
2954	LIB24-085-Q1-E1-D12	snf2_n(HMM:1e-20)
2955	20132_1.R1010	snf2_n(HMM:2.2e-05)
2956	1328372	snf2_n(HMM:2.3e-26)
2957	LIB3234-006-P1-K1-H1	snf2_n(HMM:3.1e-11)
2958	LIB23-012-Q1-E1-G1	snf2_n(HMM:3e-11)
2959	LIB24-019-Q1-E1-H9	snf2_n(HMM:4.9e-11)
2960	28253_1.R1010	srf-tf(HMM:1.1e-31)
2961	5431_1.R1010	srf-tf(HMM:1.1e-34)
2962	jC-atXLIB327403P3h07b1	srf-tf(HMM:1.4e-07)
2963	LIB25-111-Q1-E1-C9	srf-tf(HMM:1.5e-07)
2964	LIB3177-085-P1-K1-G5	srf-tf(HMM:2.9e-35)
2965	14225_2.R1010	srf-tf(HMM:2e-29)
2966	14225_3.R1010	srf-tf(HMM:2e-29)
2967	30922_1.R1010	srf-tf(HMM:3.3e-36)
2968	jC-atX24119Q1E1A11b1	srf-tf(HMM:3e-10)
2969	2733904	srf-tf(HMM:4.6e-23)
2970	30922_2.R1010	srf-tf(HMM:4.9e-07)
2971	LIB24-045-Q1-E1-F2	srf-tf(HMM:5.2e-05)
2972	26694_1.R1010	srf-tf(HMM:5.5e-18)
2973	4714014	srf-tf(HMM:6.1e-13)
2974	LIB25-016-Q1-E1-F11	srf-tf(HMM:7.5e-38)
2975	26442_1.R1010	srf-tf(HMM:9.8e-33)
2976	jC-atXP96C249I5T7b1	tbp(HMM:1.2e-38)
2977	1249_2.R1010	tbp(HMM:1.5e-81)
2978	1249_1.R1010	tbp(HMM:1.9e-80)
2979	LIB3234-033-P1-K1-H1	teo(HMM:0.0019)

2980	jC-atXP86CG9F1T7b1	teo(HMM:0.0043)
2981	jC-atXP86CG9F1T7d2	teo(HMM:0.006)
2982	1768_1.R1010	teo(HMM:1.5e-41)
2983	jC-atXLIB327414P2c10a1	teo(HMM:1.6e-25)
2984	LIB3234-095-P1-K1-H10	teo(HMM:1.9e-17)
2985	14761_1.R1010	teo(HMM:2.1e-36)
2986	2763426	teo(HMM:2.3e-16)
2987	46854_1.R1010	teo(HMM:2.4e-19)
2988	16107_1.R1010	teo(HMM:3.1e-11)
2989	33449_1.R1010	teo(HMM:3.1e-38)
2990	27952_1.R1010	teo(HMM:3.5e-36)
2991	8400_2.R1010	teo(HMM:4.1e-10)
2992	36908_1.R1010	teo(HMM:6.2e-44)
2993	7511_1.R1010	teo(HMM:7.3e-36)
2994	7171_1.R1010	teo(HMM:8.2e-33)
2995	16530_1.R1010	teo(HMM:9.7e-36)
2996	2413898	tfiis(HMM:0.015)
2997	LIB23-027-Q1-E1-E11	tfiis(HMM:3.6e-06)
2998	1343_2.R1010	transcript_fac2(HMM:0.1)
2999	35455_1.R1010	transcript_fac2(HMM:0.28)
3000	1343_1.R1010	transcript_fac2(HMM:3.1e-57)
3001	1271_1.R1010	transcript_fac2(HMM:4.1e-59)
3002	jC-atX22014Q1E1C12a1	trihelix(HMM:0.0014)
3003	103841_1.R1010	trihelix(HMM:0.0024)
3004	2393630	trihelix(HMM:0.0031)
3005	78762_1.R1010	trihelix(HMM:0.028)
3006	jC-atXLIB327418P1a10b1	trihelix(HMM:0.88)
3007	189_1.R1010	trihelix(HMM:1.2e-118)
3008	LIB146-020-Q1-E1-E3	trihelix(HMM:1.2e-12)
3009	852_1.R1010	trihelix(HMM:1.6e-56)
3010	191_1.R1010	trihelix(HMM:2.3e-120)
3011	24518_1.R1010	trihelix(HMM:2.6e-07)
3012	LIB24-135-Q1-E1-H4	trihelix(HMM:3.4e-53)
3013	27618_1.R1010	trihelix(HMM:4.3e-07)
3014	LIB24-003-Q1-E1-D5	trihelix(HMM:5.8)
3015	5312_1.R1010	trihelix(HMM:6.1e-39)
3016	22425_1.R1010	trihelix(HMM:7e-05)
3017	191_2.R1010	trihelix(HMM:8.6e-46)
3018	jC-atXLIB327411P3d07b1	wrky(HMM:0.0026)
3019	5826_1.R1010	wrky(HMM:0.0031)
3020	8539_1.R1010	wrky(HMM:0.0039)
3021	56239_1.R1010	wrky(HMM:0.015)
3022	LIB3168-082-P1-K1-E5	wrky(HMM:0.02)
3023	LIB3168-019-P1-K1-F2	wrky(HMM:0.16)
3024	LIB3177-019-P1-K2-B10	wrky(HMM:0.21)
3025	88718_1.R1010	wrky(HMM:0.27)
3026	2393545	wrky(HMM:0.34)
3027	LIB3175-020-P1-K1-G2	wrky(HMM:1.1e-05)
3028	jC-atXLIB327406P2b07a1	wrky(HMM:1.1e-22)
3029	1527_1.R1010	wrky(HMM:1.2e-40)
3030	jC-atXP39C161C17T7s1	wrky(HMM:1.4e-26)
3031	81064_1.R1010	wrky(HMM:1.6e-41)
3032	9804_1.R1010	wrky(HMM:1.6e-74)
3033	1327735	wrky(HMM:1.7e-05)

3034	118163_1.R1010	wrky(HMM:1.7e-29)
3035	LIB22-006-Q1-E1-G11	wrky(HMM:1.9e-08)
3036	14802_1.R1010	wrky(HMM:1.9e-35)
3037	5013_1.R1010	wrky(HMM:1.9e-38)
3038	LIB22-075-Q1-E1-H8	wrky(HMM:2.2e-09)
3039	jC-atXP119C193G18T7012a1	wrky(HMM:2.3e-43)
3040	jC-atXP15C106F16T7018a1	wrky(HMM:2.3e-45)
3041	2393223	wrky(HMM:2.4e-40)
3042	15470_1.R1010	wrky(HMM:2.8e-29)
3043	2759396	wrky(HMM:2e-28)
3044	1479_2.R1010	wrky(HMM:3.1e-86)
3045	jC-atXLIB327406P1d05b1	wrky(HMM:3.2e-35)
3046	LIB3175-048-P1-K1-B6	wrky(HMM:3.9e-35)
3047	56239_4.R1010	wrky(HMM:4.1e-06)
3048	56539_1.R1010	wrky(HMM:4.1e-38)
3049	73241_1.R1010	wrky(HMM:4.3e-24)
3050	2501_1.R1010	wrky(HMM:4.4e-39)
3051	LIB3176-030-P1-K1-B12	wrky(HMM:4.5e-16)
3052	773507	wrky(HMM:4e-35)
3053	93888_1.R1010	wrky(HMM:5.1e-42)
3054	102356_1.R1010	wrky(HMM:6.6e-13)
3055	1932911	wrky(HMM:7.4e-06)
3056	jC-atXP92C249D20T7085d1	wrky(HMM:7.4e-07)
3057	jC-atXP15C107M17T7066a1	wrky(HMM:7.8e-05)
3058	31824_1.R1010	wrky(HMM:8.3e-41)
3059	9668_1.R1010	"zf-b_box(HMM:0.00016),zf-constans(HMM:1.6e-33)"
3060	193_1.R1010	"zf-b_box(HMM:0.0044),zf-constans(HMM:2.7e-43)"
3061	5722_1.R1010	"zf-b_box(HMM:0.0063),zf-constans(HMM:8.4e-42)"
3062	LIB35-042-Q1-E1-A4	"zf-b_box(HMM:0.0063),zf-constans(HMM:8.4e-42)"
3063	LIB25-027-Q1-E1-H4	"zf-b_box(HMM:0.013),zf-constans(HMM:3.3e-08)"
3064	40_1.R1010	"zf-b_box(HMM:0.017),zf-constans(HMM:8.1e-42)"
3065	122486_1.R1010	"zf-b_box(HMM:0.028),zf-constans(HMM:5.6e-20)"
3066	PLN_g1161513	"zf-b_box(HMM:0.033),zf-constans(HMM:2.1e-40)"
3067	125594_2.R1010	"zf-b_box(HMM:0.039),zf-constans(HMM:3.5e-15)"
3068	51413_1.R1010	"zf-b_box(HMM:0.039),zf-constans(HMM:3.6e-26)"
3069	29526_1.R1010	"zf-b_box(HMM:0.042),zf-constans(HMM:7.6e-18)"
3070	1234_1.R1010	"zf-b_box(HMM:0.045),zf-constans(HMM:1.7e-41)"
3071	13583_1.R1010	"zf-b_box(HMM:0.053),zf-constans(HMM:3.7e-16)"
3072	17975_1.R1010	"zf-b_box(HMM:0.06),zf-constans(HMM:1.1e-17)"
3073	15190_1.R1010	"zf-b_box(HMM:0.063),zf-

		constans(HMM:2.4e-15)"
3074	jC-atXLIB327431P4f03a1	"zf-b_box(HMM:0.083),zf-constans(HMM:2.9e-31)"
3075	47411_1.R1010	"zf-b_box(HMM:0.096),zf-constans(HMM:2e-36)"
3076	24889_2.R1010	zf-c2h2(HMM:0.00051)
3077	27999_1.R1010	zf-c2h2(HMM:0.00064)
3078	jC-atXP82CG2D11T7b1	zf-c2h2(HMM:0.00067)
3079	10874_2.R1010	zf-c2h2(HMM:0.00069)
3080	970_1.R1010	zf-c2h2(HMM:0.0013)
3081	LIB3168-010-P1-K1-G9	zf-c2h2(HMM:0.0018)
3082	45108_2.R1010	zf-c2h2(HMM:0.004)
3083	80711_2.R1010	zf-c2h2(HMM:0.0074)
3084	jC-atXLIB327420P3h07b1	zf-c2h2(HMM:0.015)
3085	PLN_g790676	zf-c2h2(HMM:0.027)
3086	971_1.R1010	zf-c2h2(HMM:0.064)
3087	jC-atXP5C89H13T7036a1	zf-c2h2(HMM:0.064)
3088	969_1.R1010	zf-c2h2(HMM:0.072)
3089	PLN_g790672	zf-c2h2(HMM:0.072)
3090	PLN_g790674	zf-c2h2(HMM:0.072)
3091	8669_1.R1010	zf-c2h2(HMM:1.2e-11)
3092	PLN_g1418340	zf-c2h2(HMM:1.6e-07)
3093	1605_1.R1010	zf-c2h2(HMM:1.9e-09)
3094	1203_1.R1010	zf-c2h2(HMM:2.2e-06)
3095	5716_1.R1010	zf-c2h2(HMM:2e-05)
3096	1202_1.R1010	zf-c2h2(HMM:3.6e-08)
3097	PLN_g1418334	zf-c2h2(HMM:3.6e-08)
3098	101520_1.R1010	zf-c2h2(HMM:3.9e-09)
3099	1201_1.R1010	zf-c2h2(HMM:4.5e-10)
3100	80711_1.R1010	zf-c2h2(HMM:8.2e-12)
3101	1204_1.R1010	zf-c2h2(HMM:8.8e-09)
3102	460754	zf-c3hc4(HMM:0.00013)
3103	LIB3234-033-P1-K1-D11	zf-c3hc4(HMM:0.00013)
3104	77239_1.R1010	zf-c3hc4(HMM:0.00023)
3105	51315_1.R1010	zf-c3hc4(HMM:0.00028)
3106	1788_1.R1010	zf-c3hc4(HMM:0.00032)
3107	ARABL1-043-Q1-B1-B10	zf-c3hc4(HMM:0.00038)
3108	61662_1.R1010	zf-c3hc4(HMM:0.0004)
3109	65486_1.R1010	zf-c3hc4(HMM:0.00054)
3110	11806_1.R1010	zf-c3hc4(HMM:0.00066)
3111	2757852	zf-c3hc4(HMM:0.00077)
3112	8493_1.R1010	zf-c3hc4(HMM:0.00099)
3113	1520701	zf-c3hc4(HMM:0.0012)
3114	jC-atX24064Q1E1E05a1	zf-c3hc4(HMM:0.0015)
3115	115546_1.R1010	zf-c3hc4(HMM:0.002)
3116	76250_1.R1010	zf-c3hc4(HMM:0.0022)
3117	4272_5.R1010	zf-c3hc4(HMM:0.0024)
3118	46964_1.R1010	zf-c3hc4(HMM:0.0024)
3119	LIB3176-071-P1-K1-F4	zf-c3hc4(HMM:0.0026)
3120	150482_1.R1010	zf-c3hc4(HMM:0.003)
3121	jC-atXP101CE1E10T7058b1	zf-c3hc4(HMM:0.003)
3122	101734_1.R1010	zf-c3hc4(HMM:0.0033)
3123	jC-atXLIB327436P1g09b1	zf-c3hc4(HMM:0.0054)
3124	LIB35-037-Q1-E1-D7	zf-c3hc4(HMM:0.0054)

3125	13089_1.R1010	zf-c3hc4(HMM:0.0064)
3126	458787	zf-c3hc4(HMM:0.0084)
3127	115761_1.R1010	zf-c3hc4(HMM:0.0084)
3128	88598_1.R1010	zf-c3hc4(HMM:0.0099)
3129	LIB3176-086-P1-K1-F8	zf-c3hc4(HMM:0.011)
3130	77842_1.R1010	zf-c3hc4(HMM:0.015)
3131	88394_1.R1010	zf-c3hc4(HMM:0.015)
3132	LIB25-094-Q1-E1-B8	zf-c3hc4(HMM:0.015)
3133	LIB35-055-Q1-E2-H12	zf-c3hc4(HMM:0.015)
3134	26804_1.R1010	zf-c3hc4(HMM:0.017)
3135	44005_1.R1010	zf-c3hc4(HMM:0.019)
3136	39331_1.R1010	zf-c3hc4(HMM:0.023)
3137	96673_1.R1010	zf-c3hc4(HMM:0.024)
3138	jC-atX24005Q1E1C11a1	zf-c3hc4(HMM:0.03)
3139	634831	zf-c3hc4(HMM:0.036)
3140	33548_1.R1010	zf-c3hc4(HMM:0.041)
3141	33887_1.R1010	zf-c3hc4(HMM:0.044)
3142	213_23.R1010	zf-c3hc4(HMM:0.048)
3143	jC-atXLIB327410P2h09a1	zf-c3hc4(HMM:0.049)
3144	116810_1.R1010	zf-c3hc4(HMM:0.06)
3145	85162_1.R1010	zf-c3hc4(HMM:0.061)
3146	88872_1.R1010	zf-c3hc4(HMM:0.063)
3147	5688_2.R1010	zf-c3hc4(HMM:0.065)
3148	25145_1.R1010	zf-c3hc4(HMM:0.067)
3149	jC-atXLIB327434P4h12a1	zf-c3hc4(HMM:0.068)
3150	LIB3177-067-P1-K1-F10	zf-c3hc4(HMM:0.069)
3151	16046_1.R1010	zf-c3hc4(HMM:0.072)
3152	LIB23-027-Q1-E1-H9	zf-c3hc4(HMM:0.075)
3153	64121_1.R1010	zf-c3hc4(HMM:0.08)
3154	91568_1.R1010	zf-c3hc4(HMM:0.085)
3155	906835	zf-c3hc4(HMM:0.11)
3156	75883_1.R1010	zf-c3hc4(HMM:0.17)
3157	LIB35-042-Q1-E1-B5	zf-c3hc4(HMM:0.22)
3158	79742_3.R1010	zf-c3hc4(HMM:0.25)
3159	2749609	zf-c3hc4(HMM:0.32)
3160	13387_1.R1010	zf-c3hc4(HMM:0.55)
3161	36130_1.R1010	zf-c3hc4(HMM:0.66)
3162	104041_1.R1010	zf-c3hc4(HMM:1.1e-05)
3163	40473_1.R1010	zf-c3hc4(HMM:1.1e-07)
3164	15228_1.R1010	zf-c3hc4(HMM:1.1e-09)
3165	714_1.R1010	"zf-c3hc4(HMM:1.1e-16),zz(HMM:4.4e-16)"
3166	jC-atXLIB327436P1g09a1	zf-c3hc4(HMM:1.2e-09)
3167	2763784	zf-c3hc4(HMM:1.4e-08)
3168	70486_1.R1010	zf-c3hc4(HMM:1.4e-08)
3169	28736_1.R1010	zf-c3hc4(HMM:1.4e-09)
3170	1793_1.R1010	zf-c3hc4(HMM:1.5e-12)
3171	74196_1.R1010	zf-c3hc4(HMM:1.6e-06)
3172	1785_1.R1010	zf-c3hc4(HMM:1.6e-11)
3173	jC-atX24027Q1E1F03a1	zf-c3hc4(HMM:1.6e-11)
3174	LIB22-004-Q1-E1-D10	zf-c3hc4(HMM:1.6e-11)
3175	2413955	zf-c3hc4(HMM:1.6e-12)
3176	8878_1.R1010	zf-c3hc4(HMM:1.7e-10)
3177	7144_1.R1010	zf-c3hc4(HMM:1.7e-11)

3178	jC-atXP13C103O3T7004a1	zf-c3hc4(HMM:1.8e-07)
3179	1786_1.R1010	zf-c3hc4(HMM:1.8e-09)
3180	LIB3176-051-P1-K1-H2	zf-c3hc4(HMM:1.8e-10)
3181	14579_1.R1010	zf-c3hc4(HMM:1e-11)
3182	jC-atXLIB327409P4h04a1	zf-c3hc4(HMM:2.1)
3183	79397_1.R1010	zf-c3hc4(HMM:2.1e-11)
3184	2062852	zf-c3hc4(HMM:2.2)
3185	jC-atXLIB327438P3e01a2	zf-c3hc4(HMM:2.2e-09)
3186	1795_1.R1010	zf-c3hc4(HMM:2.3e-09)
3187	2048291	zf-c3hc4(HMM:2.3e-10)
3188	1789_1.R1010	zf-c3hc4(HMM:2.4e-14)
3189	905856	zf-c3hc4(HMM:2.5e-06)
3190	88949_1.R1010	zf-c3hc4(HMM:2.6e-13)
3191	1787_1.R1010	zf-c3hc4(HMM:2.7e-10)
3192	101518_1.R1010	zf-c3hc4(HMM:2e-10)
3193	LIB23-028-Q1-E1-C3	zf-c3hc4(HMM:3.1e-06)
3194	jC-atXP1C64A5T7s2	zf-c3hc4(HMM:3.1e-07)
3195	74854_1.R1010	zf-c3hc4(HMM:3.1e-09)
3196	ARABL1-038-Q1-E1-G10	zf-c3hc4(HMM:3.1e-11)
3197	LIB3168-061-P1-K1-A9	zf-c3hc4(HMM:3.2e-10)
3198	1794_1.R1010	zf-c3hc4(HMM:3.3e-08)
3199	128642_1.R1010	zf-c3hc4(HMM:3.4e-05)
3200	jC-atXU104f1	zf-c3hc4(HMM:3.4e-05)
3201	10177_1.R1010	zf-c3hc4(HMM:3.4e-06)
3202	15228_2.R1010	zf-c3hc4(HMM:3.4e-10)
3203	8186_1.R1010	zf-c3hc4(HMM:3.7e-06)
3204	jC-atXLIB327431P4h03a1	zf-c3hc4(HMM:3.8e-07)
3205	24635_1.R1010	zf-c3hc4(HMM:3.9e-08)
3206	22255_1.R1010	zf-c3hc4(HMM:3.9e-09)
3207	1159615	zf-c3hc4(HMM:4.2e-09)
3208	2581694	zf-c3hc4(HMM:4.2e-10)
3209	jC-atXP69C219A23T7014d1	zf-c3hc4(HMM:4.2e-10)
3210	17051_1.R1010	zf-c3hc4(HMM:4.4e-08)
3211	1874_1.R1010	zf-c3hc4(HMM:4.5e-08)
3212	1792_1.R1010	zf-c3hc4(HMM:5.5e-09)
3213	6103_1.R1010	zf-c3hc4(HMM:5.8e-07)
3214	14617_1.R1010	zf-c3hc4(HMM:6.3e-10)
3215	2754_2.R1010	zf-c3hc4(HMM:6.4e-09)
3216	101364_1.R1010	zf-c3hc4(HMM:6.4e-10)
3217	jC-atXLIB327436P2d05a1	zf-c3hc4(HMM:6.5e-05)
3218	24834_1.R1010	zf-c3hc4(HMM:6.5e-11)
3219	4922_1.R1010	zf-c3hc4(HMM:6.6e-08)
3220	15369_1.R1010	zf-c3hc4(HMM:6.8e-12)
3221	949655	zf-c3hc4(HMM:7.1e-07)
3222	96498_1.R1010	zf-c3hc4(HMM:7.4e-08)
3223	74370_1.R1010	zf-c3hc4(HMM:7.8e-06)
3224	jC-atXLIB327408P4e09a1	zf-c3hc4(HMM:7.8e-10)
3225	396_1.R1010	zf-c3hc4(HMM:7e-11)
3226	10338_1.R1010	zf-c3hc4(HMM:8.1e-07)
3227	2047468	zf-c3hc4(HMM:8.2e-05)
3228	88616_1.R1010	zf-c3hc4(HMM:8.6e-09)
3229	2581616	zf-c3hc4(HMM:8.8e-08)
3230	213_12.R1010	zf-c3hc4(HMM:8.8e-08)
3231	128926_1.R1010	zf-c3hc4(HMM:8.8e-09)

3232	jC-atXP8C92K1T7d1	zf-c3hc4(HMM:8.8e-12)
3233	47105_1.R1010	zf-c3hc4(HMM:8e-07)
3234	57820_1.R1010	zf-c3hc4(HMM:8e-12)
3235	127383_1.R1010	zf-c3hc4(HMM:9.2e-13)
3236	31344_1.R1010	zf-c3hc4(HMM:9.4e-06)
3237	1790_1.R1010	zf-c3hc4(HMM:9.7e-12)
3238	19591_1.R1010	zf-ccch(HMM:0.00014)
3239	22324_1.R1010	zf-ccch(HMM:0.00034)
3240	32632_1.R1010	zf-ccch(HMM:0.00038)
3241	11605_1.R1010	zf-ccch(HMM:0.0018)
3242	7176_1.R1010	zf-ccch(HMM:0.0023)
3243	LIB3234-087-Q1-K1-G12	zf-ccch(HMM:0.0095)
3244	20290_1.R1010	zf-ccch(HMM:0.0096)
3245	116042_1.R1010	zf-ccch(HMM:0.015)
3246	99257_1.R1010	zf-ccch(HMM:0.031)
3247	jC-atXP31C147B23T7s1	zf-ccch(HMM:0.031)
3248	jC-atXLIB327416P3e02a1	zf-ccch(HMM:0.04)
3249	LIB146-022-Q1-E1-E5	zf-ccch(HMM:0.046)
3250	1695_1.R1010	zf-ccch(HMM:0.098)
3251	116035_1.R1010	zf-ccch(HMM:1.5e-05)
3252	5626_1.R1010	zf-ccch(HMM:2.1e-06)
3253	8921_1.R1010	zf-ccch(HMM:2.1e-06)
3254	38040_1.R1010	zf-ccch(HMM:6.6e-16)
3255	1199_1.R1010	zf-cchc(HMM:0.00024)
3256	670_1.R1010	zf-cchc(HMM:0.0003)
3257	129921_1.R1010	zf-cchc(HMM:0.00053)
3258	jC-atXLIB327433P2a10a1	zf-cchc(HMM:0.0017)
3259	108675_1.R1010	zf-cchc(HMM:0.012)
3260	LIB3177-077-P1-K1-E7	zf-cchc(HMM:0.15)
3261	1200_1.R1010	zf-cchc(HMM:1.2e-05)
3262	22484_1.R1010	zf-cchc(HMM:1.5e-06)
3263	11483_1.R1010	zf-cchc(HMM:1.5e-17)
3264	LIB3176-047-P1-K1-D4	zf-cchc(HMM:1.7e-12)
3265	2763645	zf-cchc(HMM:2.6e-06)
3266	13021_1.R1010	zf-cchc(HMM:2.9e-11)
3267	129234_1.R1010	zf-cchc(HMM:4.1e-15)
3268	3418_1.R1010	zf-cchc(HMM:4.5e-05)
3269	LIB3176-069-P1-K1-H8	zf-constans(HMM:0.00032)
3270	47549_1.R1010	zf-constans(HMM:1.3e-14)
3271	28795_1.R1010	zf-constans(HMM:1.8e-31)
3272	74055_1.R1010	zf-constans(HMM:1.9e-16)
3273	315827	zf-constans(HMM:1e-10)
3274	28040_1.R1010	zf-constans(HMM:1e-25)
3275	131318_1.R1010	zf-constans(HMM:2.1e-18)
3276	7711_1.R1010	zf-constans(HMM:2.3e-14)
3277	2733155	zf-constans(HMM:2.7e-12)
3278	13864_8.R1010	zf-constans(HMM:3.3e-10)
3279	13864_3.R1010	zf-constans(HMM:3.9e-31)
3280	906416	zf-constans(HMM:4.8e-38)
3281	35325_1.R1010	zf-constans(HMM:5.6e-36)
3282	1216676	zf-constans(HMM:5e-07)
3283	jC-atXN442143a1	zf-constans(HMM:9.6e-10)
3284	1159714	zf-constans(HMM:9e-20)
3285	2048672	zf-mynd(HMM:0.037)

3286	123095_1.R1010	zf-mynd(HMM:0.27)
3287	117076_1.R1010	zf-mynd(HMM:0.85)
3288	102319_2.R1010	zf-mynd(HMM:2.3e-11)
3289	93572_1.R1010	zz(HMM:0.045)
3290	2470_1.R1010	zz(HMM:5.8e-08)
3291	550153	zz(HMM:7.6e-07)

Table 4 Transcription factors from maize

SEQ NUM	SEQ ID	Family/Method/E-value
3292	LIB189-022-Q1-E1-E2.f2	14-3-3(HMM:0.00012)
3293	uC-zmflb73092h03b2.f1	14-3-3(HMM:0.00024)
3294	LIB148-011-Q1-E1-B1.f2	14-3-3(HMM:0.00066)
3295	LIB3075-054-Q1-K1-F10.f3	14-3-3(HMM:0.0011)
3296	594_8.R1011.f3	14-3-3(HMM:0.0014)
3297	9611_2.R1011.f3	14-3-3(HMM:0.0019)
3298	LIB3156-010-Q1-K1-H2.f1	14-3-3(HMM:0.0043)
3299	LIB3066-018-Q1-K1-C4.f6	14-3-3(HMM:0.0076)
3300	LIB3152-012-P1-K1-D11.f1	14-3-3(HMM:0.024)
3301	LIB3150-049-Q1-N1-C9.f3	14-3-3(HMM:0.027)
3302	uC-zmflmo17127b07b1.f2	14-3-3(HMM:0.18)
3303	LIB3079-008-Q1-K1-B7.f2	14-3-3(HMM:1.1e-08)
3304	tfd700575123.h1.f1	14-3-3(HMM:1.2)
3305	594_2.R1011.f1	14-3-3(HMM:1.4e-30)
3306	566_1.R1011.f2	14-3-3(HMM:1.4e-77)
3307	566_3.R1011.f3	14-3-3(HMM:1.5e-161)
3308	566_9.R1011.f1	14-3-3(HMM:1.5e-29)
3309	LIB3075-042-Q1-K1-C4.f1	14-3-3(HMM:1.6e-11)
3310	1410_3.R1011.f1	14-3-3(HMM:1.7e-52)
3311	731_4.R1011.f3	14-3-3(HMM:1.9e-170)
3312	LIB3159-007-Q1-K1-E7.f1	14-3-3(HMM:1e-20)
3313	LIB3075-002-Q1-K1-B12.f3	14-3-3(HMM:2.1e-07)
3314	1410_7.R1011.f2	14-3-3(HMM:2.1e-16)
3315	wen700336508.h1.f3	14-3-3(HMM:2.1e-16)
3316	1410_1.R1011.f3	14-3-3(HMM:2.2e-178)
3317	gct701175267.h1.f2	14-3-3(HMM:2.3e-35)
3318	fC-zmro700834529r1.f4	14-3-3(HMM:2.6e-06)
3319	594_9.R1011.f2	14-3-3(HMM:2.6e-13)
3320	LIB3137-033-Q1-K1-C6.f2	14-3-3(HMM:2.8e-13)
3321	LIB3150-039-Q1-N1-D12.f1	14-3-3(HMM:2.9e-06)
3322	LIB143-015-Q1-E1-B3.f2	14-3-3(HMM:3)
3323	10404_1.R1011.f3	14-3-3(HMM:3.1e-125)
3324	fC-zmro700834529f1.f1	14-3-3(HMM:3.3e-05)
3325	uC-zmroB73028d12b1.f2	14-3-3(HMM:3.5e-26)
3326	594_3.R1011.f1	14-3-3(HMM:3.7e-127)
3327	LIB3279-053-P1-K1-D2.f2	14-3-3(HMM:3.8e-32)
3328	xjt700096581.h1.f1	14-3-3(HMM:3e-30)
3329	xyt700343495.h1.f2	14-3-3(HMM:4.1e-07)
3330	LIB3150-026-Q1-N1-F5.f2	14-3-3(HMM:4.3e-07)
3331	LIB3180-012-P2-M1-C12.f1	14-3-3(HMM:4.5e-11)
3332	LIB3066-020-Q1-K1-G3.f1	14-3-3(HMM:4.6e-05)
3333	uC-zmflmo17280d02b1.f3	14-3-3(HMM:4.7e-05)
3334	xtj700378323.h1.f2	14-3-3(HMM:4.8e-07)
3335	LIB3180-017-P2-M1-F3.f1	14-3-3(HMM:4.9e-17)
3336	566_2.R1011.f3	14-3-3(HMM:4e-176)
3337	LIB3059-008-Q1-K1-C8.f1	14-3-3(HMM:5.1e-09)
3338	LIB3180-007-P2-M1-H1.f2	14-3-3(HMM:5.2e-05)
3339	uC-zmflmo17269d08b1.f2	14-3-3(HMM:5.3e-18)
3340	LIB3076-038-Q1-K1-E4.f1	14-3-3(HMM:5.4e-12)
3341	594_1.R1011.f1	14-3-3(HMM:5.4e-172)
3342	LIB3150-017-Q1-N1-B11.f2	14-3-3(HMM:5.5e-06)
3343	9611_1.R1011.f1	14-3-3(HMM:5.6e-88)

3344	159357_2.R1011.f4	14-3-3(HMM:5.7e-05)
3345	xsy700213601.h1.f2	14-3-3(HMM:5.9e-05)
3346	LIB189-013-Q1-E1-G10.f2	14-3-3(HMM:5e-08)
3347	LIB3066-009-Q1-K1-A4.f1	14-3-3(HMM:5e-09)
3348	LIB3076-026-Q1-K1-B8.f1	14-3-3(HMM:6)
3349	LIB3066-042-Q1-K1-B8.f1	14-3-3(HMM:6.1e-34)
3350	LIB3150-097-P1-N1-B9.f3	14-3-3(HMM:6.4e-16)
3351	LIB3279-014-P1-K1-E9.f3	14-3-3(HMM:6.6e-37)
3352	LIB84-028-Q1-E1-H8.f3	14-3-3(HMM:6e-05)
3353	566_13.R1011.f2	14-3-3(HMM:7.2e-12)
3354	566_22.R1011.f1	14-3-3(HMM:7.2e-12)
3355	1410_6.R1011.f1	14-3-3(HMM:7.3e-19)
3356	uwc700153165.h1.f2	14-3-3(HMM:7.4e-31)
3357	LIB3069-008-Q1-K1-A8.f1	14-3-3(HMM:7.5e-25)
3358	594_11.R1011.f3	14-3-3(HMM:7.7e-10)
3359	uC-zmflb73008g02b1.f1	14-3-3(HMM:8.4e-09)
3360	uC-zmflmo17248f03b1.f3	14-3-3(HMM:8.8e-06)
3361	1410_2.R1011.f3	14-3-3(HMM:9.1e-113)
3362	uC-zmroB73017b10b1.f3	14-3-3(HMM:9.8e-28)
3363	159326_1.R1011.f4	ank(HMM:0.00011)
3364	pmx700086003.h1.f1	ank(HMM:0.00043)
3365	141962_2.R1011.f1	ank(HMM:0.00055)
3366	820_2.R1011.f3	ank(HMM:0.0013)
3367	uC-zmflmo17029f11b1.f2	ank(HMM:0.0031)
3368	pmx700082632.h1.f1	ank(HMM:0.01)
3369	195040_2.R1011.f4	ank(HMM:0.011)
3370	nbm700469772.h1.f6	ank(HMM:0.021)
3371	104308_1.R1011.f3	ank(HMM:0.037)
3372	uC-zmroteosinte018g09b1.f1	ank(HMM:0.047)
3373	wev700404933.h1.f3	ank(HMM:0.05)
3374	gct701171021.h1.f1	ank(HMM:0.054)
3375	1726_1.R1011.f3	ank(HMM:0.085)
3376	36318_1.R1011.f3	ank(HMM:0.15)
3377	uC-zmflb73119g02b1.f5	ank(HMM:0.35)
3378	45856_2.R1011.f2	ank(HMM:0.49)
3379	68346_1.R1011.f2	ank(HMM:1.1e-05)
3380	4075_1.R1011.f5	ank(HMM:1.1e-07)
3381	11869_2.R1011.f3	ank(HMM:1.1e-40)
3382	83366_1.R1011.f2	ank(HMM:1.2e-08)
3383	64217_2.R1011.f3	ank(HMM:1.2e-15)
3384	410_1.R1011.f1	ank(HMM:1.3e-13)
3385	543_33.R1011.f2	ank(HMM:1.3e-16)
3386	117287_1.R1011.f2	ank(HMM:1.4e-07)
3387	133011_1.R1011.f5	ank(HMM:1.4e-07)
3388	4893_1.R1011.f3	ank(HMM:1.4e-23)
3389	109900_1.R1011.f2	ank(HMM:1.7e-08)
3390	LIB3150-043-Q1-N1-F3.f3	ank(HMM:1.7e-12)
3391	xjt700093366.h1.f1	ank(HMM:1.8e-07)
3392	182080_2.R1011.f5	ank(HMM:1.9e-21)
3393	56561_1.R1011.f3	ank(HMM:1e-23)
3394	xjt700093477.h1.f2	ank(HMM:2.1e-18)
3395	138593_1.R1011.f2	ank(HMM:2.2e-08)
3396	40207_1.R1011.f2	ank(HMM:2.5e-11)
3397	15021_2.R1011.f2	ank(HMM:2.6e-20)

3398	2823_1.R1011.f2	ank(HMM:2.6e-21)
3399	59015_1.R1011.f3	ank(HMM:2.6e-29)
3400	153362_1.R1011.f6	ank(HMM:2.7e-32)
3401	820_1.R1011.f1	ank(HMM:2.7e-33)
3402	64217_1.R1011.f1	ank(HMM:2e-20)
3403	35891_1.R1011.f1	ank(HMM:2e-26)
3404	312551_1.R1011.f3	ank(HMM:2e-29)
3405	237913_1.R1011.f3	ank(HMM:3.3e-05)
3406	117462_1.R1011.f3	ank(HMM:3.5e-05)
3407	hbs701184147.h1.f2	ank(HMM:3.5e-11)
3408	uC-zmflb73093c09b2.f3	ank(HMM:3.6e-11)
3409	148636_1.R1011.f3	ank(HMM:3.7e-07)
3410	280157_1.R1011.f3	ank(HMM:3.7e-09)
3411	xsy700212143.h1.f1	ank(HMM:4.2e-06)
3412	13225_1.R1011.f1	ank(HMM:4.2e-17)
3413	11923_1.R1011.f3	ank(HMM:4.2e-19)
3414	42370_1.R1011.f1	ank(HMM:4.3e-09)
3415	LIB3062-043-Q1-K1-G11.f3	ank(HMM:4.3e-15)
3416	56078_1.R1011.f3	ank(HMM:4.4e-47)
3417	LIB3079-055-Q1-K1-A7.f2	ank(HMM:4.6e-05)
3418	LIB3150-064-P1-N1-E1.f1	ank(HMM:4.6e-11)
3419	113335_1.R1011.f1	ank(HMM:4.8e-08)
3420	12732_1.R1011.f2	ank(HMM:4e-37)
3421	uC-zmflb73349e02a2.f2	ank(HMM:5.3e-11)
3422	xyt700344979.h1.f1	ank(HMM:5.4e-11)
3423	zla700380073.h1.f1	ank(HMM:5.5e-07)
3424	141967_1.R1011.f3	ank(HMM:6.4e-32)
3425	211171_1.R1011.f2	ank(HMM:6.7e-20)
3426	uC-zmflmo17339f04b1.f3	ank(HMM:6.8e-05)
3427	gwl700614359.h1.f1	ank(HMM:6e-15)
3428	166006_1.R1011.f5	ank(HMM:7.7e-16)
3429	130820_1.R1011.f3	ank(HMM:8.1e-07)
3430	45856_1.R1011.f1	ank(HMM:8.3e-33)
3431	2823_2.R1011.f2	ank(HMM:8.6e-13)
3432	uC-zmrob73012e01b1.f3	ank(HMM:8e-09)
3433	qmh700030596.f1.f3	ap2-domain(HMM:0.00022)
3434	uC-zmflmo17278e09b1.f3	ap2-domain(HMM:0.00025)
3435	153248_1.R1011.f2	ap2-domain(HMM:0.00029)
3436	uC-zmroteosinte119c10b1.f2	ap2-domain(HMM:0.00029)
3437	LIB3075-022-Q1-K1-A3.f3	ap2-domain(HMM:0.00032)
3438	LIB3150-014-Q1-N1-B12.f3	ap2-domain(HMM:0.00038)
3439	rvl700458374.h1.f3	ap2-domain(HMM:0.0027)
3440	LIB3062-027-Q1-K1-B1.f3	ap2-domain(HMM:0.0031)
3441	hbs701183475.h1.f3	ap2-domain(HMM:0.0033)
3442	g5499545.f3	ap2-domain(HMM:0.0037)
3443	LIB3076-043-Q1-K1-H9.f2	ap2-domain(HMM:0.0085)
3444	qmh700029224.f1.f3	ap2-domain(HMM:0.009)
3445	LIB3150-014-Q1-N1-B11.f2	ap2-domain(HMM:0.0091)
3446	56107_1.R1011.f2	ap2-domain(HMM:0.015)
3447	7011_1.R1011.f2	ap2-domain(HMM:0.015)
3448	354982_1.R1011.f2	ap2-domain(HMM:0.045)
3449	uC-zmflmo17132f01a1.f5	ap2-domain(HMM:0.053)
3450	105425_1.R1011.f3	ap2-domain(HMM:0.21)
3451	LIB3150-034-Q1-N1-F5.f3	ap2-domain(HMM:0.21)

3452	LIB3279-060-P1-K1-B2.f3	ap2-domain(HMM:0.78)
3453	kem700610879.h1.f3	ap2-domain(HMM:0.89)
3454	LIB3078-051-Q1-K1-C6.f1	ap2-domain(HMM:1.1)
3455	LIB3066-002-Q1-K1-E6.f2	ap2-domain(HMM:1.1e-27)
3456	LIB143-064-Q1-E1-H9.f3	ap2-domain(HMM:1.2e-09)
3457	115159_1.R1011.f2	ap2-domain(HMM:1.2e-12)
3458	14954_2.R1011.f1	ap2-domain(HMM:1.2e-33)
3459	57898_1.R1011.f2	ap2-domain(HMM:1.4e-15)
3460	pmx700086814.h1.f3	ap2-domain(HMM:1.4e-18)
3461	LIB83-014-Q1-E1-E11.f1	ap2-domain(HMM:1.4e-30)
3462	LIB84-013-Q1-E1-H4.f1	ap2-domain(HMM:1.4e-32)
3463	LIB3115-032-P1-K1-F11.f1	ap2-domain(HMM:1.5e-31)
3464	94442_1.R1011.f3	ap2-domain(HMM:1.5e-34)
3465	fC-zmst700620948a1.f2	ap2-domain(HMM:1.6e-26)
3466	uC-zmflmo17073g07b1.f3	ap2-domain(HMM:1.8e-27)
3467	151326_1.R1011.f3	ap2-domain(HMM:1.8e-36)
3468	18554_1.R1011.f1	ap2-domain(HMM:1.8e-36)
3469	11285_1.R1011.f1	ap2-domain(HMM:1.9e-29)
3470	uwc700156315.h1.f3	ap2-domain(HMM:1e-10)
3471	19862_2.R1011.f1	ap2-domain(HMM:1e-32)
3472	uC-zmflMo17067g09b1.f3	ap2-domain(HMM:2.1e-06)
3473	1134_1.R1011.f1	ap2-domain(HMM:2.1e-68)
3474	69375_1.R1011.f2	ap2-domain(HMM:2.2e-20)
3475	LIB3279-008-P1-K1-H11.f3	ap2-domain(HMM:2.3)
3476	1015_1.R1011.f2	ap2-domain(HMM:2.4e-66)
3477	uC-zmflm017207f07b1.f1	ap2-domain(HMM:2.5e-36)
3478	18_1.R1011.f3	ap2-domain(HMM:2.5e-38)
3479	21410_1.R1011.f3	ap2-domain(HMM:2.7e-39)
3480	LIB3062-015-Q1-K1-F11.f2	ap2-domain(HMM:2.7e-40)
3481	LIB3066-002-Q1-K1-D7.f3	ap2-domain(HMM:2.9e-09)
3482	LIB3066-025-Q1-K1-D10.f1	ap2-domain(HMM:2e-36)
3483	LIB3279-060-P1-K1-B7.f3	ap2-domain(HMM:3.1e-11)
3484	13324_1.R1011.f2	ap2-domain(HMM:3.1e-27)
3485	47138_1.R1011.f2	ap2-domain(HMM:3.3)
3486	LIB3062-046-Q1-K1-B1.f3	ap2-domain(HMM:3.4e-19)
3487	91505_1.R1011.f2	ap2-domain(HMM:3.4e-26)
3488	19319_1.R1011.f5	ap2-domain(HMM:3.5e-09)
3489	fC-zmst700623908a1.f2	ap2-domain(HMM:3.5e-48)
3490	18_5.R1011.f3	ap2-domain(HMM:3.7)
3491	uC-zmflMo17092h11b1.f2	ap2-domain(HMM:3.7e-05)
3492	282965_1.R1011.f1	ap2-domain(HMM:3.7e-36)
3493	788_1.R1011.f3	ap2-domain(HMM:3.7e-62)
3494	tfd700573489.h2.f2	ap2-domain(HMM:3e-41)
3495	zla700380117.h1.f3	ap2-domain(HMM:4.1)
3496	176781_1.R1011.f5	ap2-domain(HMM:4.1e-14)
3497	vux700161592.h1.f1	ap2-domain(HMM:4.2e-30)
3498	1134_2.R1011.f1	ap2-domain(HMM:4.5e-56)
3499	cjh700197716.h1.f2	ap2-domain(HMM:4.8e-37)
3500	LIB3062-042-Q1-K1-A4.f1	ap2-domain(HMM:5.1e-12)
3501	369_1.R1011.f4	ap2-domain(HMM:5.1e-38)
3502	LIB3156-001-Q1-K1-H9.f2	ap2-domain(HMM:5.3e-26)
3503	14954_1.R1011.f2	ap2-domain(HMM:5.4e-33)
3504	42286_1.R1011.f2	ap2-domain(HMM:5.6e-37)
3505	LIB3137-013-Q1-K1-H10.f3	ap2-domain(HMM:7.2e-07)

3506	173_1.R1011.f1	ap2-domain(HMM:7.2e-36)
3507	LIB3118-011-Q1-K1-B1.f2	ap2-domain(HMM:7.5e-38)
3508	19862_1.R1011.f2	ap2-domain(HMM:8.3e-39)
3509	154890_1.R1011.f1	ap2-domain(HMM:9.5e-42)
3510	40836_1.R1011.f2	ap2-domain(HMM:9.6e-37)
3511	22183_1.R1011.f5	ap2-domain(HMM:9.8e-12)
3512	45015_1.R1011.f3	ap2-domain(HMM:9.8e-41)
3513	LIB3180-047-P2-G3.f1	arf(HMM:0.00018)
3514	295090_1.R1011.f1	arf(HMM:0.00071),b3(HMM:1.1e-05)
3515	g5555419.f3	arf(HMM:0.0015)
3516	uwc700152959.h1.f3	arf(HMM:0.0049),b3(HMM:2.2e-07)
3517	uC-zmflb73175c11b1.f2	arf(HMM:0.01)
3518	121418_1.R1011.f2	arf(HMM:1.1e-48),b3(HMM:1.2e-20)
3519	123702_1.R1011.f2	arf(HMM:1.1e-49),b3(HMM:4.7e-37)
3520	40180_2.R1011.f3	arf(HMM:1.1e-81),b3(HMM:1.1e-43)
3521	20840_1.R1011.f3	arf(HMM:1.2e-18),b3(HMM:4.3e-28)
3522	59030_1.R1011.f2	arf(HMM:1.2e-19)
3523	5125_1.R1011.f3	arf(HMM:1.3e-14),b3(HMM:4.8e-08)
3524	fdz701158984.h2.f2	arf(HMM:1.3e-27),b3(HMM:0.085)
3525	LIB3076-001-Q1-K1-D4.f3	arf(HMM:1.4e-08)
3526	rvt700552571.h1.f1	arf(HMM:1.4e-13)
3527	qmh700028591.f1.f2	arf(HMM:1.6),b3(HMM:0.00064)
3528	gwl700613433.h1.f2	arf(HMM:1.6e-17)
3529	296401_1.R1011.f3	arf(HMM:1.7e-09)
3530	LIB3068-003-Q1-K1-F5.f2	arf(HMM:1.7e-12),b3(HMM:0.00011)
3531	90938_1.R1011.f1	arf(HMM:1.7e-15),iaa(HMM:3e-37)
3532	LIB3060-022-Q1-K1-E5.f3	arf(HMM:1.9e-25)
3533	uC-zmflmo17050f03b2.f1	arf(HMM:2.2e-10)
3534	pmx700088108.h1.f1	arf(HMM:2.3e-10),b3(HMM:2e-24)
3535	LIB3069-017-Q1-K1-C5.f5	arf(HMM:2.5e-07),b3(HMM:4.2e-19)
3536	36737_1.R1011.f3	arf(HMM:2.9e-17)
3537	xmt700260445.h1.f1	arf(HMM:3.1e-15)
3538	5832_1.R1011.f3	arf(HMM:3.2e-21),b3(HMM:0.11)
3539	11840_1.R1011.f3	arf(HMM:3.3e-83),b3(HMM:1.7e-16)
3540	uC-zmrob73080h10b1.f1	arf(HMM:3.6e-05)
3541	93228_1.R1011.f2	arf(HMM:3.9e-08)
3542	45125_2.R1011.f1	arf(HMM:3.9e-33)
3543	84957_1.R1011.f4	arf(HMM:4.1e-226),b3(HMM:1.2e-53)

3544	167490_1.R1011.f3	arf(HMM:4.1e-84),b3(HMM:5e-29)
3545	uC-zmroteosinte011c06b1.f1	arf(HMM:4.4)
3546	5206_1.R1011.f3	arf(HMM:4.5e-15),iaa(HMM:7.3e-42)
3547	40180_1.R1011.f6	arf(HMM:4.6e-18),b3(HMM:0.39)
3548	ymt700219207.h1.f2	arf(HMM:4.8e-07)
3549	nbm700473253.h1.f2	arf(HMM:5.5e-05),b3(HMM:1.4e-14)
3550	rvt700551414.h1.f1	arf(HMM:5.7e-22)
3551	xjt700096660.h1.f2	arf(HMM:5e-14)
3552	14342_1.R1011.f2	arf(HMM:6.5e-21),iaa(HMM:1.6e-35)
3553	xsy700212223.h1.f2	arf(HMM:8.1),b3(HMM:2.2e-13)
3554	uC-zmflmo17242d12b1.f2	arf(HMM:8.2e-11)
3555	4856_1.R1011.f3	arf(HMM:8.5e-13)
3556	136361_1.R1011.f1	arf(HMM:8.7e-15)
3557	uC-zmflmo17187e06b1.f3	arf(HMM:9.5e-13),b3(HMM:3.9e-34)
3558	uC-zmflmo17020c04b1.f2	arf(HMM:9.7e-13),b3(HMM:1.2e-08)
3559	rvt700549405.h1.f3	arf(HMM:9.9e-06),b3(HMM:7.9e-10)
3560	26695_1.R1011.f6	arid(HMM:0.012)
3561	pmx700085770.h1.f1	arid(HMM:0.067)
3562	12446_1.R1011.f2	arid(HMM:5.8e-06)
3563	61331_1.R1011.f3	athook(HMM:0.067),linker histone(HMM:4.5e-18)
3564	LIB3066-045-Q1-K1-G6.f3	b3(HMM:0.00014)
3565	cyk700051980.f1.f3	b3(HMM:0.0022)
3566	61168_1.R1011.f2	b3(HMM:1.2e-62)
3567	64730_3.R1011.f3	b3(HMM:1.8e-17)
3568	138382_1.R1011.f1	b3(HMM:1.9e-47)
3569	uC-zmflmo17150d04b1.f1	b3(HMM:2.6e-13)
3570	g2437851.f3	b3(HMM:3.8e-11)
3571	112988_1.R1011.f6	b3(HMM:3e-06)
3572	595_1.R1011.f1	b3(HMM:4.4e-72)
3573	uC-zmroteosinte109f10b3.f2	b3(HMM:5.5e-08)
3574	64730_1.R1011.f1	b3(HMM:8e-34)
3575	155104_1.R1011.f3	b3(HMM:9.8e-39)
3576	LIB3069-031-Q1-K1-A4.f1	bah(HMM:0.00023)
3577	122916_1.R1011.f2	bah(HMM:0.01)
3578	20651_1.R1011.f2	bah(HMM:1.6e-17),phd(HMM:2.6e-06)
3579	4802_1.R1011.f3	bah(HMM:1.7e-36),phd(HMM:9e-13)
3580	uC-zmflmo17280e09b1.f1	bah(HMM:1.9e-09)
3581	189689_1.R1011.f1	bah(HMM:1e-09)
3582	139677_1.R1011.f2	bah(HMM:1e-26)
3583	uC-zmroB73015h11b1.f2	bah(HMM:2.6e-30),phd(HMM:0.0085)
3584	uC-zmflb73057c03a2.f6	bah(HMM:5.1e-05)
3585	67623_1.R1011.f1	bah(HMM:8.8e-07)

3586	774_1.R1011.f1	bpf-1(HMM:0)
3587	774_2.R1011.f3	bpf-1(HMM:0)
3588	uC-zmflb73318h08b1.f1	bpf-1(HMM:3.3e-12)
3589	uC-zmflb73193b04b1.f1	bpf-1(HMM:4.2e-12)
3590	LIB3066-049-Q1-K1-B3.f2	bpf-1(HMM:4.5e-32)
3591	uC-zmflmo17187a03b1.f3	bpf-1(HMM:5.2e-13)
3592	LIB3279-059-P1-K1-C4.f1	bpf-1(HMM:7.7e-36)
3593	uC-zmflb73212e04a1.f2	bromodomain(HMM:0.00071)
3594	nbm700467939.h1.f2	bromodomain(HMM:0.0011)
3595	77245_1.R1011.f3	bromodomain(HMM:0.0019)
3596	76108_1.R1011.f3	bromodomain(HMM:0.082)
3597	ymt700223701.h1.f1	bromodomain(HMM:0.41)
3598	xjt700092623.h1.f1	bromodomain(HMM:0.55)
3599	266593_1.R1011.f1	bromodomain(HMM:1.5e-09)
3600	31955_1.R1011.f2	bromodomain(HMM:1.5e-19)
3601	pmx700090964.h1.f3	bromodomain(HMM:2.8e-22)
3602	45171_1.R1011.f1	bromodomain(HMM:4.7e-25)
3603	nwy700447086.h1.f1	bromodomain(HMM:5.4e-14)
3604	77056_1.R1011.f2	bromodomain(HMM:5e-07)
3605	66917_1.R1011.f1	bromodomain(HMM:6.1e-29)
3606	58940_1.R1011.f2	bromodomain(HMM:6.4e-12)
3607	wen700334517.h1.f3	bromodomain(HMM:7.9)
3608	12516_1.R1011.f3	bromodomain(HMM:9.5e-05)
3609	77258_1.R1011.f3	bromodomain(HMM:9.8e-32)
3610	wen700332659.h1.f1	bromodomain(HMM:9e-31)
3611	pmx700090579.h1.f2	btb(HMM:0.00013)
3612	uC-zmflmo17309d06b1.f2	btb(HMM:0.00014)
3613	94638_1.R1011.f1	btb(HMM:0.00028)
3614	wyr700242203.h1.f2	btb(HMM:0.023)
3615	LIB148-012-Q1-E1-E4.f1	btb(HMM:0.039)
3616	79402_1.R1011.f1	btb(HMM:0.083)
3617	5427_2.R1011.f4	btb(HMM:0.18)
3618	24283_1.R1011.f1	btb(HMM:1.2e-26)
3619	67288_1.R1011.f3	btb(HMM:1.4)
3620	46942_1.R1011.f1	btb(HMM:1.4e-28)
3621	56570_1.R1011.f1	btb(HMM:1.5e-20)
3622	136749_1.R1011.f3	btb(HMM:1.8e-08)
3623	230586_1.R1011.f2	btb(HMM:1.8e-08)
3624	36908_1.R1011.f2	btb(HMM:1.9e-20)
3625	vfk700404896.h1.f1	btb(HMM:1e-05)
3626	qmh700028765.f1.f3	btb(HMM:3.5)
3627	LIB189-031-Q1-E1-F6.f1	btb(HMM.4.5e-17)
3628	117075_1.R1011.f3	bzip(HMM:0.00045)
3629	19767_2.R1011.f3	bzip(HMM:0.0012)
3630	g297019.f1	bzip(HMM:0.0019)
3631	183787_1.R1011.f6	bzip(HMM:0.0021)
3632	184_1.R1011.f3	bzip(HMM:0.0023)
3633	19767_1.R1011.f2	bzip(HMM:0.0029)
3634	796_1.R1011.f3	bzip(HMM:0.0036)
3635	94067_1.R1011.f3	bzip(HMM:0.0037)
3636	LIB3078-008-Q1-K1-A8.f2	bzip(HMM:0.0046)
3637	80936_1.R1011.f3	bzip(HMM:0.0058)
3638	80936_3.R1011.f2	bzip(HMM:0.0058)
3639	66094_2.R1011.f1	bzip(HMM:0.0073)

3640	fC-zmro700834891f1.f4	bzip(HMM:0.0084)
3641	996_1.R1011.f3	bzip(HMM:0.0098)
3642	36566_1.R1011.f1	bzip(HMM:0.011)
3643	uC-zmflb73142c04b1.f1	bzip(HMM:0.011)
3644	2705_1.R1011.f3	bzip(HMM:0.014)
3645	246805_1.R1011.f1	bzip(HMM:0.015)
3646	xsy700217015.h1.f2	bzip(HMM:0.031)
3647	31891_1.R1011.f2	bzip(HMM:0.035)
3648	cyk700051876.f1.f2	bzip(HMM:0.045)
3649	80936_4.R1011.f2	bzip(HMM:0.053)
3650	168_1.R1011.f2	bzip(HMM:0.074)
3651	1894_3.R1011.f3	bzip(HMM:0.079)
3652	16253_1.R1011.f2	bzip(HMM:0.11)
3653	uC-zmflmo17113b02b1.f1	bzip(HMM:0.11)
3654	LIB83-001-Q1-E1-H6.f3	bzip(HMM:0.17)
3655	26070_2.R1011.f1	bzip(HMM:0.23)
3656	xyt700343308.h1.f1	bzip(HMM:0.25)
3657	LIB3180-035-P2-M2-D10.f2	bzip(HMM:0.42)
3658	80936_2.R1011.f3	bzip(HMM:1)
3659	LIB3156-017-Q1-K1-B12.f1	bzip(HMM:1.3)
3660	9912_2.R1011.f2	bzip(HMM:1.3e-16)
3661	6292_1.R1011.f3	bzip(HMM:1.4e-12)
3662	65710_1.R1011.f1	bzip(HMM:1.4e-12)
3663	66302_1.R1011.f3	bzip(HMM:1.5)
3664	559_1.R1011.f2	bzip(HMM:1.5e-19)
3665	559_2.R1011.f1	bzip(HMM:1.5e-19)
3666	69626_1.R1011.f3	bzip(HMM:1.6e-21)
3667	11877_1.R1011.f2	bzip(HMM:1.7)
3668	fC-zmro700807549a1.f3	bzip(HMM:1.7e-15)
3669	uC-zmflmo17240b07b1.f1	bzip(HMM:1.7e-16)
3670	uC-zmflmo17219e03b1.f3	bzip(HMM:1.8e-05)
3671	174_1.R1011.f3	bzip(HMM:1e-06)
3672	LIB3067-002-Q1-K1-D4.f3	bzip(HMM:1e-08)
3673	76804_1.R1011.f1	bzip(HMM:1e-09)
3674	35221_3.R1011.f3	bzip(HMM:2.1e-12)
3675	19923_1.R1011.f1	bzip(HMM:2.1e-15)
3676	30964_1.R1011.f1	bzip(HMM:2.2e-13)
3677	3559_2.R1011.f3	bzip(HMM:2.3e-06)
3678	875_1.R1011.f3	bzip(HMM:2.4e-21)
3679	LIB3136-025-Q1-K1-G3.f2	bzip(HMM:2.4e-21)
3680	795_1.R1011.f3	bzip(HMM:2.6e-16)
3681	uC-zmroteosinte090c12b2.f2	bzip(HMM:2.9e-10)
3682	11539_1.R1011.f1	bzip(HMM:2.9e-11)
3683	149215_1.R1011.f1	bzip(HMM:2e-05)
3684	LIB3136-008-Q1-K1-F12.f2	bzip(HMM:2e-06)
3685	62007_1.R1011.f1	bzip(HMM:2e-11)
3686	548_1.R1011.f2	bzip(HMM:3e-17)
3687	495_1.R1011.f1	bzip(HMM:4.5e-14)
3688	13140_1.R1011.f3	bzip(HMM:4.9e-07)
3689	80158_1.R1011.f1	bzip(HMM:5.1e-20)
3690	66094_1.R1011.f3	bzip(HMM:5.3e-13)
3691	93670_1.R1011.f2	bzip(HMM:5.4e-13)
3692	93670_2.R1011.f1	bzip(HMM:5.4e-13)
3693	uC-zmflMo17086c07b1.f2	bzip(HMM:5.4e-21)

3694	uC-zmflmo17023a04b1.f3	bzip(HMM:5.8e-05)
3695	12102_1.R1011.f1	bzip(HMM:6.6e-14)
3696	91750_1.R1011.f2	bzip(HMM:6.8e-08)
3697	LIB3062-026-Q1-K1-D6.f1	bzip(HMM:6.9e-21)
3698	171_1.R1011.f3	bzip(HMM:7.1e-21)
3699	qmh700028533.f1.f3	bzip(HMM:7.3e-18)
3700	111526_1.R1011.f3	bzip(HMM:7.5e-12)
3701	9912_1.R1011.f3	bzip(HMM:8.1e-17)
3702	78927_1.R1011.f2	bzip(HMM:8.2)
3703	495_2.R1011.f1	bzip(HMM:9.1e-15)
3704	uC-zmroteosinte106e02b2.f1	bzip(HMM:9.3e-15)
3705	793_4.R1011.f1	cbfd_nfyb_hmf(HMM:0.00056)
3706	cyk700048913.f1.f1	cbfd_nfyb_hmf(HMM:0.0069)
3707	3683_1.R1011.f2	cbfd_nfyb_hmf(HMM:0.1)
3708	LIB3076-053-Q1-E1-F1.f2	cbfd_nfyb_hmf(HMM:1.1e-19)
3709	8110_2.R1011.f2	cbfd_nfyb_hmf(HMM:1.5e-17)
3710	793_1.R1011.f2	cbfd_nfyb_hmf(HMM:3.3e-37)
3711	LIB3066-048-Q1-K1-B3.f1	cbfd_nfyb_hmf(HMM:3.3e-37)
3712	uC-zmflb73001e01b1.f1	cbfd_nfyb_hmf(HMM:3.5e-06)
3713	25618_1.R1011.f3	cbfd_nfyb_hmf(HMM:3.6e-27)
3714	13043_1.R1011.f3	cbfd_nfyb_hmf(HMM:5.1e-29)
3715	LIB3059-019-Q1-K1-A3.f2	cbfd_nfyb_hmf(HMM:5.9e-23)
3716	793_2.R1011.f2	cbfd_nfyb_hmf(HMM:5e-39)
3717	uwc700154561.h1.f2	cbfd_nfyb_hmf(HMM:6.4e-05)
3718	8110_1.R1011.f3	cbfd_nfyb_hmf(HMM:6.8e-19)
3719	15049_1.R1011.f1	cbfd_nfyb_hmf(HMM:6.9e-15)
3720	793_3.R1011.f2	cbfd_nfyb_hmf(HMM:9.2e-38)
3721	g5108360.f6	chromo(HMM:0.016)
3722	wty700168802.h1.f2	chromo(HMM:0.02)
3723	123177_1.R1011.f3	chromo(HMM:0.95)
3724	65108_1.R1011.f2	chromo(HMM:2.3e-18)
3725	ceu700425120.h1.f3	chromo(HMM:3.9e-05)
3726	LIB3070-015-Q1-N1-A3.f2	csd(HMM:0.0019)
3727	uC-zmflmo17270b10b1.f2	csd(HMM:1.1),zf-cchc(HMM:0.77)
3728	LIB3137-035-Q1-K1-C7.f3	csd(HMM:1.1e-17)
3729	22575_1.R1011.f2	csd(HMM:2.8e-24),zf-cchc(HMM:7.5e-16)
3730	LIB3180-013-P2-M1-D2.f1	csd(HMM:5.5e-12)
3731	28942_1.R1011.f2	csd(HMM:5e-22)
3732	LIB3180-003-P2-M1-G12.f2	csd(HMM:8.3e-20)
3733	LIB3182-004-P2-M1-E8.f1	csd(HMM:9.8e-24)
3734	LIB3159-016-Q1-K1-C5.f1	dof(HMM:0.0053)
3735	726_1.R1011.f2	dof(HMM:1.3e-34)
3736	119611_1.R1011.f1	dof(HMM:1.3e-36)
3737	76636_1.R1011.f1	dof(HMM:2.6e-35)
3738	uC-zmflmo17322b10b1.f1	dof(HMM:2.7e-35)
3739	1164_1.R1011.f1	dof(HMM:2.8e-36)
3740	348176_1.R1011.f3	dof(HMM:2.9e-05)
3741	uC-zmflmo17300d10b1.f2	dof(HMM:6.4e-12)
3742	725_1.R1011.f3	dof(HMM:7e-32)
3743	789_1.R1011.f2	dof(HMM:7e-33)
3744	36684_1.R1011.f3	dof(HMM:8e-08)
3745	83493_1.R1011.f2	dpb(HMM:0.00088)

3746	7415_3.R1011.f2	dpb(HMM:0.0052)
3747	109657_1.R1011.f2	dpb(HMM:0.012)
3748	17195_2.R1011.f2	dpb(HMM:0.025)
3749	fxb700397533.h1.f2	dpb(HMM:0.059)
3750	7415_2.R1011.f3	dpb(HMM:0.07)
3751	42447_1.R1011.f3	dpb(HMM:1.4)
3752	7415_4.R1011.f2	dpb(HMM:1.5e-05)
3753	9825_2.R1011.f3	dpb(HMM:1e-06)
3754	109498_1.R1011.f3	dpb(HMM:3.4e-05)
3755	uC-zmflb73098h12b1.f3	dpb(HMM:3.4e-07)
3756	LIB3137-040-Q1-K1-F12.f2	dpb(HMM:3.6e-16)
3757	8830_1.R1011.f3	dpb(HMM:3.7e-52)
3758	7415_1.R1011.f3	dpb(HMM:3.9e-74)
3759	7415_5.R1011.f3	dpb(HMM:4.5)
3760	8830_2.R1011.f1	dpb(HMM:4.6e-17)
3761	9825_1.R1011.f1	dpb(HMM:8.7e-10)
3762	uC-zmroteosinte053e10b2.f2	enbp(HMM:0.00091)
3763	175089_1.R1011.f6	enbp(HMM:0.23)
3764	4_3.R1011.f1	enbp(HMM:2.5e-05)
3765	25860_1.R1011.f3	enbp(HMM:3.1e-26)
3766	uC-zmroteosinte038a09b1.f6	enbp(HMM:3e-08)
3767	g4646558.f2	enbp(HMM:3e-21)
3768	ceu700433052.h1.f3	enbp(HMM:4.4e-06)
3769	rvt700551738.h1.f1	enbp(HMM:4.4e-21)
3770	LIB3059-014-Q1-K1-D1.f2	enbp(HMM:4.6e-06)
3771	uC-zmflmo17300a10b1.f3	enbp(HMM:5.9e-21)
3772	90700_1.R1011.f2	enbp(HMM:7.1e-15)
3773	LIB3115-030-P1-K1-C5.f1	enbp(HMM:9.7e-21)
3774	xyt700344683.h1.f2	gata(HMM:0.00021)
3775	5422_1.R1011.f2	gata(HMM:0.0017)
3776	g5608102.f4	gata(HMM:0.024)
3777	92655_1.R1011.f3	gata(HMM:1.2e-15)
3778	g5439296.f5	gata(HMM:1.6e-11)
3779	LIB3076-047-Q1-K1-G3.f3	gata(HMM:1.7e-07)
3780	LIB3136-044-P1-K1-H10.f2	gata(HMM:1.7e-15)
3781	uC-zmflb73054c10b1.f3	gata(HMM:1e-09)
3782	1852_1.R1011.f3	gata(HMM:3e-06)
3783	42120_1.R1011.f6	gata(HMM:4.3e-08)
3784	42120_2.R1011.f5	gata(HMM:4.3e-08)
3785	10646_1.R1011.f1	gata(HMM:4.5e-15)
3786	362_1.R1011.f4	gata(HMM:4.9e-15)
3787	ypc700804682.h1.f2	gata(HMM:7.7e-06)
3788	LIB3180-020-P2-M1-D3.f1	gata(HMM:9.6e-15)
3789	dyk700105142.h1.f2	gld-tea(HMM:0.00036)
3790	83829_1.R1011.f2	gld-tea(HMM:0.00063)
3791	uC-zmflb73199e11b1.f3	gld-tea(HMM:0.0042)
3792	LIB3070-013-Q1-N1-F11.f1	gld-tea(HMM:0.0067)
3793	LIB3150-031-Q1-N1-H9.f1	gld-tea(HMM:0.011)
3794	LIB3068-026-Q1-K1-C9.f1	gld-tea(HMM:0.013),myb_dna-binding(HMM:1.5e-11)
3795	wyr700239235.h1.f3	gld-tea(HMM:0.05)
3796	56327_1.R1011.f3	gld-tea(HMM:0.087)
3797	111218_2.R1011.f2	gld-tea(HMM:0.17)
3798	LIB3150-045-Q1-N1-E10.f2	gld-tea(HMM:0.33)

3799	111218_1.R1011.f2	gld-tea(HMM:0.64)
3800	11928_1.R1011.f2	gld-tea(HMM:1.2e-31)
3801	g5740668.f1	gld-tea(HMM:1.3e-29)
3802	106032_1.R1011.f3	gld-tea(HMM:1.3e-30)
3803	9580_1.R1011.f2	gld-tea(HMM:1.3e-36)
3804	uC-zmflb73195h02b1.f1	gld-tea(HMM:1.8)
3805	9580_2.R1011.f3	gld-tea(HMM:1.8e-31)
3806	g5607837.f5	gld-tea(HMM:1e-28)
3807	233343_1.R1011.f3	gld-tea(HMM:2.1e-17)
3808	63245_1.R1011.f1	gld-tea(HMM:2.3e-19)
3809	LIB3136-049-Q1-K1-D5.f2	gld-tea(HMM:3.1e-31)
3810	ypc700804994.h1.f2	gld-tea(HMM:3.1e-34)
3811	22554_1.R1011.f2	gld-tea(HMM:4.2e-29)
3812	127865_1.R1011.f3	gld-tea(HMM:4.4e-30)
3813	wen700332259.h1.f1	gld-tea(HMM:4.9e-07)
3814	wyr700239376.h1.f1	gld-tea(HMM:5.4e-27)
3815	LIB3088-004-Q1-K1-A4.f2	gld-tea(HMM:5.9e-12)
3816	15271_1.R1011.f3	gld-tea(HMM:6.2e-24)
3817	yyf700349742.h1.f1	gld-tea(HMM:8.3)
3818	117481_1.R1011.f1	gld-tea(HMM:9.1e-36)
3819	12948_1.R1011.f3	hhh(HMM:3.6e-05)
3820	1052_1.R1011.f2	hhh(HMM:3e-08)
3821	1053_1.R1011.f1	hhh(HMM:9.2e-07)
3822	dyk700102440.h1.f2	hist_deacetyl(HMM:0.00015)
3823	uC-zmflmo17050g12b2.f2	hist_deacetyl(HMM:0.00038)
3824	LIB3152-001-Q1-K1-B2.f2	hist_deacetyl(HMM:1.1e-10)
3825	30591_1.R1011.f3	hist_deacetyl(HMM:1.2e-146)
3826	ceu700432474.h1.f1	hist_deacetyl(HMM:1.3)
3827	187025_1.R1011.f2	hist_deacetyl(HMM:1.8e-10)
3828	200741_1.R1011.f3	hist_deacetyl(HMM:1e-10)
3829	6786_1.R1011.f2	hist_deacetyl(HMM:1e-37)
3830	1011_1.R1011.f1	hist_deacetyl(HMM:2.2e-160)
3831	72749_1.R1011.f2	hist_deacetyl(HMM:2.8e-51)
3832	cyk700047402.f1.f1	hist_deacetyl(HMM:3.5e-15)
3833	rvl700454171.h1.f2	hist_deacetyl(HMM:4.6e-11)
3834	994_1.R1011.f3	hist_deacetyl(HMM:6e-181)
3835	304250_1.R1011.f2	hist_deacetyl(HMM:8.9e-09)
3836	3274_1.R1011.f2	hist_deacetyl(HMM:8.9e-123)
3837	LIB3150-049-Q1-N1-F11.f1	hist_deacetyl(HMM:8e-10)
3838	g4804054.f5	histone(HMM:0.00011)
3839	uwc700151004.h1.f3	histone(HMM:0.00017)
3840	LIB3150-071-P1-N1-E2.f1	histone(HMM:0.00023)
3841	xyt700343992.h1.f2	histone(HMM:0.00027)
3842	LIB3279-011-P1-K1-F2.f1	histone(HMM:0.00035)
3843	LIB3079-035-Q1-K1-D5.f3	histone(HMM:0.00045)
3844	LIB3070-005-Q1-N1-G9.f2	histone(HMM:0.0005)
3845	LIB3059-017-Q1-K1-H2.f1	histone(HMM:0.00058)
3846	LIB3067-018-Q1-K1-F2.f2	histone(HMM:0.00065)
3847	286579_1.R1011.f1	histone(HMM:0.00069)
3848	LIB3150-075-P1-N1-G7.f3	histone(HMM:0.00077)
3849	cat700021823.r1.f6	histone(HMM:0.00083)
3850	865_21.R1011.f3	histone(HMM:0.00084)
3851	yyf700348078.h1.f3	histone(HMM:0.00086)
3852	LIB3150-083-P2-N2-D11.f6	histone(HMM:0.00093)

3853	292487_1.R1011.f2	histone(HMM:0.00099)
3854	cat700020406.r1.f2	histone(HMM:0.0013)
3855	cjh700195179.h1.f2	histone(HMM:0.0014)
3856	LIB3068-026-Q1-K1-F8.f3	histone(HMM:0.0014)
3857	uC-zmflb73177e01b1.f3	histone(HMM:0.002)
3858	g5688683.f6	histone(HMM:0.0024)
3859	dyk700104373.h1.f2	histone(HMM:0.0026)
3860	LIB3070-010-Q1-N1-H2.f1	histone(HMM:0.003)
3861	LIB3150-029-Q1-N1-H11.f1	histone(HMM:0.0032)
3862	LIB3088-050-Q1-K1-G10.f3	histone(HMM:0.0035)
3863	wen700333394.h1.f1	histone(HMM:0.0035)
3864	LIB3150-078-P2-N2-D8.f1	histone(HMM:0.0037)
3865	pmx700085984.h1.f2	histone(HMM:0.0041)
3866	LIB3150-002-Q1-N1-C10.f3	histone(HMM:0.0045)
3867	LIB3067-004-Q1-K1-G12.f2	histone(HMM:0.005)
3868	ymt700219717.h1.f3	histone(HMM:0.005)
3869	g4630548.f6	histone(HMM:0.0052)
3870	yyf700349869.h1.f1	histone(HMM:0.0055)
3871	pmx700088257.h1.f3	histone(HMM:0.007)
3872	cyk700052421.f1.f3	histone(HMM:0.0074)
3873	xjt700094901.h1.f6	histone(HMM:0.008)
3874	LIB3116-028-P1-K1-C8.f1	histone(HMM:0.0091)
3875	LIB3088-041-Q1-K1-D8.f1	histone(HMM:0.0097)
3876	gwl700612741.h1.f3	histone(HMM:0.016)
3877	LIB3078-019-Q1-K1-H11.f3	histone(HMM:0.016)
3878	LIB3088-044-Q1-K1-D2.f2	histone(HMM:0.017)
3879	LIB3279-054-P1-K1-D6.f3	histone(HMM:0.017)
3880	LIB3279-055-P1-K1-D2.f2	histone(HMM:0.017)
3881	LIB3150-050-Q1-N1-E6.f1	histone(HMM:0.018)
3882	LIB3158-017-Q1-K1-G9.f1	histone(HMM:0.018)
3883	LIB3088-044-Q1-K1-B10.f2	histone(HMM:0.02)
3884	rvt700553369.h1.f2	histone(HMM:0.022)
3885	uC-zmflb73032h09b1.f2	histone(HMM:0.022)
3886	338_9.R1011.f3	histone(HMM:0.024)
3887	95_13.R1011.f1	histone(HMM:0.025)
3888	LIB3070-014-Q1-N1-C4.f1	histone(HMM:0.028)
3889	LIB148-064-Q1-E1-B9.f1	histone(HMM:0.029)
3890	cat700019176.r1.f1	histone(HMM:0.031)
3891	95_12.R1011.f2	histone(HMM:0.033)
3892	cat700019288.r1.f3	histone(HMM:0.042)
3893	pmx700089077.h1.f1	histone(HMM:0.056)
3894	LIB84-022-Q1-E1-D1.f3	histone(HMM:0.057)
3895	xmt700257966.h1.f2	histone(HMM:0.062)
3896	LIB3078-038-Q1-K1-B2.f3	histone(HMM:0.072)
3897	LIB143-057-Q1-E1-D9.f1	histone(HMM:0.074)
3898	ckd700461156.h1.f2	histone(HMM:0.078)
3899	LIB3279-014-P1-K1-D8.f1	histone(HMM:0.078)
3900	95_9.R1011.f1	histone(HMM:0.1)
3901	vux700158357.h1.f2	histone(HMM:0.1)
3902	xjt700094748.h1.f1	histone(HMM:0.1)
3903	cat700020560.r1.f2	histone(HMM:0.11)
3904	dyk700103145.h1.f2	histone(HMM:0.12)
3905	LIB3067-008-Q1-K1-H9.f3	histone(HMM:0.13)
3906	wen700333417.h1.f1	histone(HMM:0.14)

3907	95_22.R1011.f2	histone(HMM:0.17)
3908	LIB3076-019-Q1-K1-A2.f3	histone(HMM:0.17)
3909	LIB3150-081-P1-N1-G2.f2	histone(HMM:0.2)
3910	95_17.R1011.f3	histone(HMM:0.27)
3911	LIB3059-054-Q1-K1-B5.f2	histone(HMM:0.3)
3912	qmh700027751.f1.f1	histone(HMM:0.31)
3913	666_1.R1011.f6	histone(HMM:0.37)
3914	LIB3279-011-P1-K1-H6.f2	histone(HMM:0.4)
3915	LIB3150-043-Q1-N1-C10.f3	histone(HMM:0.49)
3916	LIB3070-004-Q1-N1-G12.f1	histone(HMM:0.5)
3917	LIB3088-044-Q1-K1-A3.f3	histone(HMM:0.85)
3918	95_23.R1011.f2	histone(HMM:0.93)
3919	LIB3088-011-Q1-K1-G7.f1	histone(HMM:0.98)
3920	xyt700346501.h1.f3	histone(HMM:0.99)
3921	757_37.R1011.f2	histone(HMM:1.1)
3922	ydl700405355.h1.f2	histone(HMM:1.1e-05)
3923	LIB3067-056-Q1-K1-F12.f3	histone(HMM:1.1e-07)
3924	LIB3150-054-Q1-N1-G11.f2	histone(HMM:1.1e-16)
3925	yyf700349182.h1.f1	histone(HMM:1.1e-16)
3926	LIB3088-042-Q1-K1-B9.f3	histone(HMM:1.1e-20)
3927	LIB3150-032-Q1-N1-G3.f1	histone(HMM:1.1e-30)
3928	g5268737.f1	histone(HMM:1.1e-37)
3929	286749_1.R1011.f3	histone(HMM:1.1e-42)
3930	757_11.R1011.f1	histone(HMM:1.1e-47)
3931	LIB3279-005-P1-K1-B7.f1	histone(HMM:1.2e-05)
3932	xyt700343350.h1.f2	histone(HMM:1.2e-08)
3933	rvl700454901.h1.f3	histone(HMM:1.2e-11)
3934	g3341056.f4	histone(HMM:1.2e-13)
3935	LIB3070-004-Q1-N1-E3.f3	histone(HMM:1.2e-13)
3936	LIB3150-052-Q1-N1-B2.f2	histone(HMM:1.2e-21)
3937	865_3.R1011.f3	histone(HMM:1.2e-51)
3938	wyr700244484.h1.f1	histone(HMM:1.3e-06)
3939	hvj700619851.h1.f2	histone(HMM:1.3e-08)
3940	LIB3076-046-Q1-K1-H11.f2	histone(HMM:1.3e-11)
3941	LIB3180-038-P2-M2-C6.f2	histone(HMM:1.3e-14)
3942	uC-zmflb73163d03a1.f5	histone(HMM:1.3e-26)
3943	757_6.R1011.f1	histone(HMM:1.3e-45)
3944	uC-zmflb73359g07a2.f3	histone(HMM:1.4e-06)
3945	uwc700153036.h1.f1	histone(HMM:1.4e-07)
3946	mwy700442376.h1.f2	histone(HMM:1.4e-08)
3947	LIB3137-005-Q1-K1-B9.f6	histone(HMM:1.4e-11)
3948	uC-zmroteosinte099g08b2.f1	histone(HMM:1.4e-16)
3949	1672_2.R1011.f2	histone(HMM:1.4e-43)
3950	g3341140.f6	histone(HMM:1.5e-24)
3951	338_13.R1011.f3	histone(HMM:1.5e-34)
3952	16775_1.R1011.f1	histone(HMM:1.5e-49)
3953	25582_1.R1011.f6	histone(HMM:1.5e-49)
3954	LIB3150-108-P2-K1-D1.f5	histone(HMM:1.6e-08)
3955	pmx700082311.h1.f1	histone(HMM:1.6e-11)
3956	LIB3070-012-Q1-N1-A8.f3	histone(HMM:1.6e-18)
3957	757_8.R1011.f1	histone(HMM:1.6e-46)
3958	865_1.R1011.f2	histone(HMM:1.6e-52)
3959	ckd700461256.h1.f2	histone(HMM:1.7e-05)
3960	LIB143-037-Q1-E1-H1.f3	histone(HMM:1.7e-05)

3961	LIB3150-040-Q1-N1-A10.f3	histone(HMM:1.7e-05)
3962	LIB3156-011-Q1-K1-C2.f1	histone(HMM:1.7e-06)
3963	41834_1.R1011.f2	histone(HMM:1.7e-07)
3964	LIB3150-064-P1-N1-A5.f1	histone(HMM:1.7e-17)
3965	LIB3150-035-Q1-N1-E2.f2	histone(HMM:1.7e-30)
3966	uC-zmroteosinte051e09b2.f3	histone(HMM:1.7e-46)
3967	757_3.R1011.f2	histone(HMM:1.7e-47)
3968	xmt700256940.h1.f2	histone(HMM:1.8e-06)
3969	yyf700352343.h1.f1	histone(HMM:1.8e-14)
3970	uC-zmflb73306e04b1.f3	histone(HMM:1.8e-18)
3971	uC-zmroteosinte059e07b1.f3	histone(HMM:1.8e-32)
3972	757_32.R1011.f1	histone(HMM:1.9e-06)
3973	pmx700083528.h1.f1	histone(HMM:1.9e-06)
3974	cat700021164.r1.f3	histone(HMM:1.9e-08)
3975	LIB3059-042-Q1-K1-F2.f1	histone(HMM:1.9e-08)
3976	LIB3067-014-Q1-K1-D10.f1	histone(HMM:1.9e-08)
3977	ymt700224008.h1.f1	histone(HMM:1.9e-13)
3978	LIB3150-016-Q1-N1-G3.f1	histone(HMM:1.9e-14)
3979	LIB3279-011-P1-K1-H2.f3	histone(HMM:1.9e-16)
3980	hvj700618938.h1.f2	histone(HMM:1.9e-17)
3981	g3341036.f4	histone(HMM:1.9e-41)
3982	g5268911.f3	histone(HMM:1.9e-46)
3983	xsy700214625.h1.f1	histone(HMM:1e-05)
3984	LIB3088-046-Q1-K1-H2.f2	histone(HMM:1e-11)
3985	338_12.R1011.f1	histone(HMM:1e-29)
3986	LIB3279-010-P1-K1-E6.f2	histone(HMM:1e-32)
3987	15994_1.R1011.f1	histone(HMM:1e-49)
3988	wyr700235659.h1.f3	histone(HMM:2.1)
3989	LIB3062-034-Q1-K1-D11.f1	histone(HMM:2.1e-10)
3990	95_6.R1011.f2	histone(HMM:2.1e-18)
3991	g3341043.f5	histone(HMM:2.1e-37)
3992	865_6.R1011.f3	histone(HMM:2.1e-51)
3993	LIB3150-038-Q1-N1-C5.f2	histone(HMM:2.2e-07)
3994	xyt700344851.h1.f3	histone(HMM:2.2e-07)
3995	7649_2.R1011.f1	histone(HMM:2.2e-09)
3996	LIB3076-024-Q1-K1-B7.f2	histone(HMM:2.2e-43)
3997	1792_2.R1011.f3	histone(HMM:2.2e-46)
3998	757_17.R1011.f3	histone(HMM:2.2e-48)
3999	LIB3150-052-Q1-N1-G11.f2	histone(HMM:2.3e-12)
4000	757_42.R1011.f3	histone(HMM:2.3e-40)
4001	qmh700029402.f1.f1	histone(HMM:2.4)
4002	LIB3069-011-Q1-K1-F6.f2	histone(HMM:2.4e-05)
4003	LIB3076-005-Q1-K1-D5.f1	histone(HMM:2.4e-07)
4004	LIB3079-036-Q1-K1-D4.f1	histone(HMM:2.4e-10)
4005	g4776119.f5	histone(HMM:2.4e-14)
4006	LIB3137-005-Q1-K1-G10.f1	histone(HMM:2.4e-19)
4007	865_4.R1011.f5	histone(HMM:2.4e-50)
4008	757_20.R1011.f2	histone(HMM:2.5e-07)
4009	LIB3067-042-Q1-K1-B11.f2	histone(HMM:2.5e-17)
4010	LIB3150-107-P1-N1-B4.f3	histone(HMM:2.5e-18)
4011	LIB3137-016-Q1-K1-H12.f1	histone(HMM:2.6)
4012	2026_7.R1011.f6	histone(HMM:2.6e-10)
4013	yyf700347416.h1.f1	histone(HMM:2.6e-20)
4014	1792_1.R1011.f1	histone(HMM:2.6e-46)

4015	338_3.R1011.f2	histone(HMM:2.6e-46)
4016	338_7.R1011.f3	histone(HMM:2.6e-46)
4017	8267_1.R1011.f1	histone(HMM:2.6e-46)
4018	LIB3153-005-Q1-K1-H1.f1	histone(HMM:2.7e-10)
4019	LIB143-049-Q1-E1-H1.f2	histone(HMM:2.7e-11)
4020	LIB3088-049-Q1-K1-A5.f3	histone(HMM:2.7e-14)
4021	338_1.R1011.f2	histone(HMM:2.7e-45)
4022	16775_2.R1011.f2	histone(HMM:2.7e-49)
4023	LIB3078-052-Q1-K1-H1.f3	histone(HMM:2.8e-09)
4024	LIB3150-013-Q1-N1-B10.f3	histone(HMM:2.8e-09)
4025	LIB36-021-Q1-E1-G2.f2	histone(HMM:2.8e-09)
4026	LIB3067-013-Q1-K1-B1.f3	histone(HMM:2.8e-10)
4027	LIB3069-049-Q1-K1-E1.f3	histone(HMM:2.8e-13)
4028	LIB3137-005-Q1-K1-A12.f4	histone(HMM:2.8e-23)
4029	757_2.R1011.f1	histone(HMM:2.8e-46)
4030	LIB3279-059-P1-K1-H8.f3	histone(HMM:2.9e-06)
4031	cat700017931.r1.f3	histone(HMM:2e-06)
4032	LIB3067-001-Q1-K1-A4.f2	histone(HMM:2e-11)
4033	pwr700449415.h1.f1	histone(HMM:2e-11)
4034	uC-zmflB73006d03b1.f1	histone(HMM:2e-20)
4035	wty700164347.h1.f3	histone(HMM:3.1e-09)
4036	dyk700105350.h1.f2	histone(HMM:3.2e-06)
4037	cat700020669.r1.f3	histone(HMM:3.2e-07)
4038	757_44.R1011.f3	histone(HMM:3.2e-28)
4039	865_2.R1011.f1	histone(HMM:3.2e-51)
4040	865_7.R1011.f2	histone(HMM:3.2e-51)
4041	865_8.R1011.f3	histone(HMM:3.2e-51)
4042	uwc700150016.h1 f2	histone(HMM:3.3e-06)
4043	ceu700426183.h1.f1	histone(HMM:3.3e-10)
4044	g5058937.f5	histone(HMM:3.4e-22)
4045	6594_1.R1011.f2	histone(HMM:3.4e-49)
4046	LIB3076-004-Q1-K1-D1.f2	histone(HMM:3.4e-49),phd(HMM:0.11)
4047	15342_1.R1011.f2	histone(HMM:3.5e-15)
4048	g5713880.f5	histone(HMM:3.5e-24)
4049	757_5.R1011.f1	histone(HMM:3.5e-46)
4050	338_26.R1011.f1	histone(HMM:3.6e-08)
4051	LIB3079-053-Q1-K1-D2.f3	histone(HMM:3.6e-14)
4052	95_10.R1011.f2	histone(HMM:3.6e-15)
4053	757_36.R1011.f3	histone(HMM:3.6e-25)
4054	60399_1.R1011.f1	histone(HMM:3.7e-11)
4055	uC-zmflb73018h09b1.f1	histone(HMM:3.7e-45)
4056	757_14.R1011.f1	histone(HMM:3.7e-47)
4057	tzu700206634.h1.f3	histone(HMM:3.8e-07)
4058	pwr700453322.h1.f3	histone(HMM:3.8e-11)
4059	ntr700073403.h1.f2	histone(HMM:3.8e-14)
4060	757_25.R1011 f1	histone(HMM:3.8e-41)
4061	666_5.R1011.f6	histone(HMM:3.8e-44)
4062	LIB3088-009-Q1-K1-G8.f1	histone(HMM:3.9e-12)
4063	LIB3279-013-P1-K1-H3.f2	histone(HMM:3.9e-23)
4064	LIB3070-014-Q1-N1-C11.f1	histone(HMM:3e-07)
4065	95_8.R1011.f1	histone(HMM:4.1e-18)
4066	LIB3150-075-P1-N1-F7.f1	histone(HMM:4.2e-09)
4067	LIB3059-047-Q1-K1-H1.f2	histone(HMM.4.2e-17)

4068	uC-zmflb73193g04b1.f3	histone(HMM:4.2e-29)
4069	757_16.R1011.f2	histone(HMM:4.3e-47)
4070	zla700380212.h1.f3	histone(HMM:4.4)
4071	dyk700106733.h1.f1	histone(HMM:4.4e-06)
4072	LIB3088-050-Q1-K1-C2.f2	histone(HMM:4.4e-07)
4073	vux700160627.h1.f1	histone(HMM:4.4e-11)
4074	865_16.R1011.f6	histone(HMM:4.4e-15)
4075	ntr700074528.h1.f3	histone(HMM:4.5e-37)
4076	g5268696.f2	histone(HMM:4.5e-40)
4077	757_12.R1011.f1	histone(HMM:4.5e-46)
4078	vux700158183.h1.f1	histone(HMM:4.6e-05)
4079	uC-zmflB73025e02b2.f3	histone(HMM:4.6e-11)
4080	LIB3153-005-Q1-K1-B5.f3	histone(HMM:4.7e-05)
4081	yyf700349642.h1.f2	histone(HMM:4.7e-07)
4082	qmh700028985.f1.f1	histone(HMM:4.7e-11)
4083	757_7.R1011.f1	histone(HMM:4.7e-46)
4084	uC-zmflmo170114e10b1.f3	histone(HMM:4.8e-44)
4085	95_11.R1011.f3	histone(HMM:4.9e-08)
4086	LIB3070-005-Q1-N1-B3.f3	histone(HMM:4.9e-13)
4087	LIB3076-044-Q1-K1-G3.f3	histone(HMM:4e-05)
4088	338_16.R1011.f1	histone(HMM:4e-06)
4089	xmt700261612.h1.f3	histone(HMM:4e-06)
4090	LIB3088-003-Q1-K1-A3.f1	histone(HMM:4e-18)
4091	uC-zmflmo17336b11b1.f1	histone(HMM:4e-34)
4092	865_9.R1011.f1	histone(HMM:4e-42)
4093	1672_1.R1011.f1	histone(HMM:4e-45)
4094	wty700172957.h1.f2	histone(HMM:5.1e-07)
4095	g3341197.f2	histone(HMM:5.1e-08)
4096	865_12.R1011.f3	histone(HMM:5.1e-23)
4097	354331_1.R1011.f3	histone(HMM:5.2e-05)
4098	LIB148-002-Q1-E1-B12.f1	histone(HMM:5.2e-08)
4099	LIB3076-021-Q1-K1-F8.f2	histone(HMM:5.2e-37)
4100	xyt700346422.h1.f1	histone(HMM:5.3e-13)
4101	865_14.R1011.f6	histone(HMM:5.3e-49)
4102	hvj700621760.h1.f1	histone(HMM:5.6e-06)
4103	LIB3180-060-P2-M1-H6.f3	histone(HMM:5.6e-06)
4104	LIB3279-051-P1-K1-C7.f2	histone(HMM:5.6e-06)
4105	LIB3078-007-Q1-K1-F11.f1	histone(HMM:5.6e-11)
4106	gwl700613664.h1.f2	histone(HMM:5.6e-12)
4107	uC-zmflb73178a01b1.f2	histone(HMM:5.6e-14)
4108	uC-zmroteosinte102h01b2.f3	histone(HMM:5.6e-21)
4109	cyk700051888.f1.f1	histone(HMM:5.7e-06)
4110	g3340926.f5	histone(HMM:5.8e-05)
4111	tfd700572124.h1.f2	histone(HMM:5.8e-11)
4112	kem700610759.h1.f3	histone(HMM:5.9e-10)
4113	zla700379678.h1.f1	histone(HMM:5.9e-11)
4114	LIB3150-112-P2-K1-C2.f4	histone(HMM:5e-07)
4115	g3341037.f6	histone(HMM:5e-20)
4116	g3341089.f5	histone(HMM:6 1e-07)
4117	tfd700569151.h1.f2	histone(HMM:6.1e-12)
4118	LIB143-063-Q1-E1-D12.f2	histone(HMM:6.1e-16)
4119	xsy700214944.h1.f3	histone(HMM:6.3e-06)
4120	zla700380613.h1.f3	histone(HMM:6.3e-11)
4121	LIB3180-019-P2-M1-B1.f2	histone(HMM:6.3e-17)

4122	gwl700618137.h1.f3	histone(HMM:6.5e-07)
4123	LIB3116-025-P1-K2-F8.f2	histone(HMM:6.6)
4124	LIB3088-036-Q1-K1-H8.f2	histone(HMM:6.6e-06)
4125	LIB3069-003-Q1-K1-G4.f1	histone(HMM:6.6e-10)
4126	g3341079.f5	histone(HMM:6.6e-35)
4127	g548036.f2	histone(HMM:6.7e-14)
4128	757_18.R1011.f2	histone(HMM:6.7e-34)
4129	LIB3070-010-Q1-N1-G7.f1	histone(HMM:6.8e-06)
4130	cat700016831.r2.f3	histone(HMM:6.9e-15)
4131	uC-zmroteosinte030d12b1.f1	histone(HMM:6.9e-16)
4132	LIB3059-049-Q1-K1-E4.f3	histone(HMM:6.9e-29)
4133	LIB3076-029-Q1-K1-F10.f1	histone(HMM:6.9e-30)
4134	g3341041.f4	histone(HMM:6.9e-45)
4135	LIB3088-011-Q1-K1-D5.f3	histone(HMM:7.1e-09)
4136	95_21.R1011.f1	histone(HMM:7.2)
4137	757_19.R1011.f2	histone(HMM:7.2e-42)
4138	338_10.R1011.f1	histone(HMM:7.3e-41)
4139	338_22.R1011.f3	histone(HMM:7.3e-44)
4140	1672_5.R1011.f3	histone(HMM:7.4e-12)
4141	LIB3069-035-Q1-K1-E2.f1	histone(HMM:7.5)
4142	LIB143-046-Q1-E1-C10.f3	histone(HMM:7.6e-13)
4143	338_6.R1011.f2	histone(HMM:7.6e-46)
4144	LIB3076-004-Q1-K1-A11.f1	histone(HMM:7.9e-06)
4145	wyr700238913.h1.f1	histone(HMM:7.9e-07)
4146	hvj700619294.h1.f1	histone(HMM:7.9e-08)
4147	338_23.R1011.f2	histone(HMM:7.9e-44)
4148	15544_1.R1011.f1	histone(HMM:7e-20)
4149	g5650399.f5	histone(HMM:8.1e-15)
4150	1166_2.R1011.f2	histone(HMM:8.1e-51)
4151	1677_1.R1011.f1	histone(HMM:8.1e-51)
4152	qmh700027322.f1.f1	histone(HMM:8.3e-07)
4153	757_1.R1011.f3	histone(HMM:8.3e-47)
4154	uC-zmflB73112h02b2.f1	histone(HMM:8.4e-08)
4155	uC-zmflmo17297e08b1.f3	histone(HMM:8.4e-37)
4156	LIB3137-005-Q1-K1-G9.f2	histone(HMM:8.6e-07)
4157	pmx700088408.h1.f2	histone(HMM:8.6e-07)
4158	pmx700086025.h1.f2	histone(HMM:8.7e-05)
4159	1672_8.R1011.f1	histone(HMM:8.7e-09)
4160	LIB3076-018-Q1-K1-E6.f2	histone(HMM:8.7e-11)
4161	LIB3067-046-Q1-K1-H9.f1	histone(HMM:8.7e-12)
4162	865_5.R1011.f1	histone(HMM:8.7e-52)
4163	LIB3062-027-Q1-K1-E12.f1	histone(HMM:8.9e-05)
4164	LIB3069-008-Q1-K1-A11.f5	histone(HMM:8.9e-09)
4165	5857_1.R1011.f3	histone(HMM:8e-07)
4166	uC-zmrob73075d01b1.f2	histone(HMM:8e-14)
4167	LIB3116-025-P1-K1-F8.f1	histone(HMM:9.3)
4168	LIB3069-048-Q1-K1-A1.f2	histone(HMM:9.3e-33)
4169	LIB3279-004-P1-K1-H7.f3	histone(HMM:9.7e-09)
4170	6074_1.R1011.f1	histone(HMM:9.7e-51)
4171	g4572905.f4	histone(HMM:9.8)
4172	LIB3079-041-Q1-K1-C3.f1	histone(HMM:9.8e-09)
4173	338_14.R1011.f1	histone(HMM:9.9e-47)
4174	338_5.R1011.f1	histone(HMM:9.9e-47)
4175	uC-zmflb73028d10b1.f3	histone(HMM:9.9e-47)

4176	tzu700205503.h1.f1	histone(HMM:9e-12)
4177	wty700168638.h1.f3	hlh(HMM:0.00026)
4178	pmx700085722.h1.f1	hlh(HMM:0.00033)
4179	7914_1.R1011.f1	hlh(HMM:0.0056)
4180	9442_2.R1011.f2	hlh(HMM:0.013)
4181	uC-zmflb73012g11b1.f2	hlh(HMM:0.013)
4182	245026_1.R1011.f1	hlh(HMM:0.02)
4183	40548_1.R1011.f2	hlh(HMM:0.034)
4184	80197_1.R1011.f1	hlh(HMM:0.036)
4185	133275_1.R1011.f1	hlh(HMM:0.041)
4186	fdz701165182.h1.f3	hlh(HMM:0.046)
4187	133245_1.R1011.f1	hlh(HMM:0.048)
4188	wyr700237155.h1.f2	hlh(HMM:0.049)
4189	14440_1.R1011.f2	hlh(HMM:0.052)
4190	214046_1.R1011.f3	hlh(HMM:0.058)
4191	10605_1.R1011.f2	hlh(HMM:0.063)
4192	106370_1.R1011.f2	hlh(HMM:0.063)
4193	cat700021841.r1.f3	hlh(HMM:0.076)
4194	uC-zmflB73002a04b1.f1	hlh(HMM:0.076)
4195	104405_1.R1011.f1	hlh(HMM:0.084)
4196	78856_2.R1011.f3	hlh(HMM:0.086)
4197	qmh700028639.f1.f3	hlh(HMM:0.089)
4198	LIB3067-055-Q1-K1-E3.f3	hlh(HMM:0.099)
4199	g4887525.f4	hlh(HMM:0.11)
4200	fwa700100255.h1.f2	hlh(HMM:0.31)
4201	nbm700468724.h1.f3	hlh(HMM:0.69)
4202	uC-zmflb73099d02b1.f1	hlh(HMM:0.74)
4203	155010_1.R1011.f3	hlh(HMM:1.1e-12)
4204	11328_1.R1011.f3	hlh(HMM:1.5e-07)
4205	uC-zmflmo17131c08a1.f4	hlh(HMM:1.5e-12)
4206	9274_1.R1011.f3	hlh(HMM:1.7e-09)
4207	LIB3156-002-Q1-K1-A12.f2	hlh(HMM:1.8)
4208	246596_1.R1011.f5	hlh(HMM:1.9e-09)
4209	42580_1.R1011.f3	hlh(HMM:1.9e-12)
4210	11613_1.R1011.f3	hlh(HMM:1e-05)
4211	47991_1.R1011.f1	hlh(HMM:1e-09)
4212	xyt700342458.h1.f2	hlh(HMM:2.1e-06)
4213	324352_1.R1011.f1	hlh(HMM:2.1e-09)
4214	tzu700206189.h1.f2	hlh(HMM:2.1e-13)
4215	45993_1.R1011.f2	hlh(HMM:2e-16)
4216	277222_1.R1011.f1	hlh(HMM:3.3e-09)
4217	165141_1.R1011.f2	hlh(HMM:3.4e-10)
4218	593_1.R1011.f1	hlh(HMM:3.6e-14)
4219	593_2.R1011.f1	hlh(HMM:3.6e-14)
4220	1032_1.R1011.f1	hlh(HMM:5.2e-15)
4221	LIB3088-037-Q1-K1-E11.f2	hlh(HMM:5.9e-05)
4222	g22194.f1	hlh(HMM:6.3e-16)
4223	5983_1.R1011.f3	hlh(HMM:6.8e-12)
4224	158887_1.R1011.f4	hlh(HMM:6.9e-11)
4225	68023_1.R1011.f3	hlh(HMM:7.7e-09)
4226	LIB3069-006-Q1-K1-C11.f2	hlh(HMM:8.5e-16)
4227	22182_1.R1011.f2	hlh(HMM:8.9e-06)
4228	6061_1.R1011.f2	hlh(HMM:9.4e-07)
4229	uwc700155775.h1.f1	hlh(HMM:9.5e-06)

4230	104151_1.R1011.f1	hlh(HMM:9.9e-09)
4231	LIB143-063-Q1-E1-G12.f1	hmg_box(HMM:0.0017)
4232	xjt700092660.h1.f1	hmg_box(HMM:0.0018)
4233	xsy700213026.h1.f2	hmg_box(HMM:0.0018)
4234	uC-zmflmo17218b08a1.f6	hmg_box(HMM:0.0019)
4235	1116_2.R1011.f3	hmg_box(HMM:0.02)
4236	zuv700354730.h1.f1	hmg_box(HMM:0.089)
4237	LIB3059-029-Q1-K1-B11.f3	hmg_box(HMM:0.15)
4238	uwc700155406.h1.f2	hmg_box(HMM:0.23)
4239	hvj700620934.h1.f2	hmg_box(HMM:0.54)
4240	52173_1.R1011.f1	hmg_box(HMM:0.59)
4241	16250_1.R1011.f3	hmg_box(HMM:1.2e-24)
4242	34113_1.R1011.f2	hmg_box(HMM:1.4e-06)
4243	rvl700457875.h1.f1	hmg_box(HMM:1.5e-15)
4244	201269_2.R1011.f1	hmg_box(HMM:1.5e-19)
4245	762_3.R1011.f1	hmg_box(HMM:1.6e-18)
4246	2748_1.R1011.f1	hmg_box(HMM:1.8e-18)
4247	762_1.R1011.f2	hmg_box(HMM:1.9e-29)
4248	LIB3150-071-P1-N1-H11.f3	hmg_box(HMM:2.1e-07)
4249	34113_2.R1011.f1	hmg_box(HMM:2.1e-20)
4250	LIB3151-003-Q1-K1-F11.f2	hmg_box(HMM:2.6e-06)
4251	33323_1.R1011.f3	hmg_box(HMM:2.6e-20)
4252	8194_1.R1011.f1	hmg_box(HMM:3.2e-26)
4253	uC-zmflb73040a04b1.f3	hmg_box(HMM:3e-27)
4254	uC-zmroteosinte068b05b1.f2	hmg_box(HMM:4.3e-12)
4255	yyf700348989.h1.f1	hmg_box(HMM:4.4e-28)
4256	763_1.R1011.f3	hmg_box(HMM:5.1e-30)
4257	xyt700346708.h1.f3	hmg_box(HMM:5.1e-30)
4258	760_4.R1011.f1	hmg_box(HMM:5.6e-29)
4259	LIB3076-007-Q1-K1-H11.f1	hmg_box(HMM:6.1e-21)
4260	763_5.R1011.f2	hmg_box(HMM:6.5e-27)
4261	LIB3067-045-Q1-K1-C4.f2	hmg_box(HMM:6.9e-24)
4262	762_4.R1011.f2	hmg_box(HMM:7.8e-27)
4263	1116_1.R1011.f3	hmg_box(HMM:8.1e-13)
4264	760_1.R1011.f3	hmg_box(HMM:8.5e-29)
4265	201269_1.R1011.f2	hmg_box(HMM:8.6e-10)
4266	388_11.R1011.f4	homeobox(HMM:0.00014)
4267	780_1.R1011.f3	homeobox(HMM:0.00043),homeobox_knox3(1.5e-34)
4268	33684_1.R1011.f2	homeobox(HMM:0.00058),homeobox_knox3(5.6e-10)
4269	135329_1.R1011.f2	homeobox(HMM:0.001),homeobox_knox3(4.6e-34)
4270	206382_1.R1011.f2	homeobox(HMM:0.0019),homeobox_knox3(1.4e-11),homeobox_mat(0.0002)
4271	uC-zmflb73084b12b2.f3	homeobox(HMM:0.0031),homeobox_knox3(5.6e-13)
4272	175_1.R1011.f2	homeobox(HMM:0.0032)
4273	LIB3066-028-Q1-K1-E9.f2	homeobox(HMM:0.0033)
4274	uC-zmflmo17306a12b1.f3	homeobox(HMM:0.0033)
4275	17_1.R1011.f2	homeobox(HMM:0.0056),phd(HMM:1.2e-11)
4276	LIB3137-018-Q1-K1-B10.f2	homeobox(HMM:0.0071)

4277	154608_1.R1011.f2	homeobox(HMM:0.0081),homeobox_knox3(5.6e-12)
4278	LIB3067-032-Q1-K1-F8.f1	homeobox(HMM:0.0085),homeobox_knox3(2.0e-12)
4279	55031_1.R1011.f3	homeobox(HMM:0.01)
4280	ymt700219170.h1.f3	homeobox(HMM:0.014),homeobox_knox3(9.3e-13),homeobox_mat(8.1e-05)
4281	8191_1.R1011.f2	homeobox(HMM:0.016),homeobox_knox3(2.6e-22)
4282	uC-zmflmo17364h11a1.f6	homeobox(HMM:0.017),homeobox_knox3(4.3e-13)
4283	62412_1.R1011.f3	homeobox(HMM:0.017),homeobox_knox3(5.9e-12)
4284	93311_1.R1011.f1	homeobox(HMM:0.022),homeobox_knox3(3.2e-22)
4285	wyr700241308.h1.f2	homeobox(HMM:0.031),homeobox_knox3(9.2e-08)
4286	69814_2.R1011.f2	homeobox(HMM:0.062)
4287	7310_1.R1011.f3	homeobox(HMM:0.094),homeobox_knox3(3.5e-09)
4288	25970_1.R1011.f6	homeobox(HMM:0.1),homeobox_knox3(2.7e-20)
4289	LIB3066-043-Q1-K1-D10.f3	homeobox(HMM:0.26)
4290	uC-zmflb73252d04b3.f1	homeobox(HMM:0.29)
4291	uC-zmflMo17002e04b1.f1	homeobox(HMM:0.29)
4292	LIB3062-052-Q1-K1-B9.f2	homeobox(HMM:1)
4293	388_3.R1011.f6	homeobox(HMM:1.4e-19)
4294	388_2.R1011.f6	homeobox(HMM:1.4e-20)
4295	fC-zmfl700549125f3.f1	homeobox(HMM:1.5)
4296	128072_1.R1011.f2	homeobox(HMM:1.7e-18)
4297	388_4.R1011.f4	homeobox(HMM:1.8e-17)
4298	LIB3136-018-Q1-K1-F8.f2	homeobox(HMM:1.9)
4299	766_2.R1011.f1	homeobox(HMM:1.9e-12),phd(HMM:2.7e-15)
4300	uC-zmflB73007b08b1.f1	homeobox(HMM:1.9e-18)
4301	388_1.R1011.f5	homeobox(HMM:1.9e-19)
4302	1067_1.R1011.f2	homeobox(HMM:2.4e-05),homeobox_knox3(2.8e-30)
4303	110797_2.R1011.f2	homeobox(HMM:2.8e-06)
4304	388_5.R1011.f5	homeobox(HMM:2e-14)
4305	69814_1.R1011.f2	homeobox(HMM:3.2e-18)
4306	11330_1.R1011.f1	homeobox(HMM:3.3e-06)
4307	154166_1.R1011.f2	homeobox(HMM:3.3e-16)
4308	187_1.R1011.f2	homeobox(HMM:3.4e-22),homeobox_knox3(0.0008)
4309	185_1.R1011.f3	homeobox(HMM:3.9e-19)
4310	764_1.R1011.f3	homeobox(HMM:3e-06),phd(HMM:4.2e-16)
4311	uC-zmflmo17020c02b1.f1	homeobox(HMM:4.1e-16)
4312	766_1.R1011.f1	homeobox(HMM:5.9e-17),phd(HMM:6.6e-16)
4313	388_6.R1011.f6	homeobox(HMM:6.4e-18)
4314	hbs701186070.h1.f1	homeobox(HMM:6.7e-06)

4315	hbs701183093.h1.f6	homeobox(HMM:7)
4316	764_2.R1011.f1	homeobox(HMM:8.3e-08).phd(HMM:8.6e-16).homeobox_knox3(0.0007)
4317	598_1.R1011.f1	homeobox(HMM:8.5e-05).homeobox_knox3(8.5e-37)
4318	8190_1.R1011.f3	homeobox(HMM:9.4e-20)
4319	LIB3137-024-Q1-K1-F4.f1	hsf_dna-bind(HMM:0.00019)
4320	7092_1.R1011.f2	hsf_dna-bind(HMM:0.0009)
4321	fdz701166808.h1.f2	hsf_dna-bind(HMM:0.0036)
4322	fdz701163214.h1.f1	hsf_dna-bind(HMM:0.0044)
4323	1729_1.R1011.f1	hsf_dna-bind(HMM:0.038)
4324	xjt700092059.h1.f2	hsf_dna-bind(HMM:0.049)
4325	46875_1.R1011.f1	hsf_dna-bind(HMM:0.056)
4326	7801_1.R1011.f3	hsf_dna-bind(HMM:1.6e-06)
4327	nwy700446322.h1.f3	hsf_dna-bind(HMM:1.6e-07)
4328	dyk700102210.h1.f2	hsf_dna-bind(HMM:1.6e-26)
4329	LIB84-028-Q1-E1-F5.f3	hsf_dna-bind(HMM:1.8e-06)
4330	154751_1.R1011.f1	hsf_dna-bind(HMM:1.8e-23)
4331	LIB189-016-Q1-E1-H8.f3	hsf_dna-bind(HMM:1.9e-20)
4332	153848_1.R1011.f3	hsf_dna-bind(HMM:2.2e-08)
4333	qmh700030486.f1.f1	hsf_dna-bind(HMM:2.3e-10)
4334	768_1.R1011.f3	hsf_dna-bind(HMM:3e-35)
4335	48395_1.R1011.f1	hsf_dna-bind(HMM:4.3e-55)
4336	fC-zmse700836407f1.f1	hsf_dna-bind(HMM:5.2e-09)
4337	dyk700106455.h1.f3	hsf_dna-bind(HMM:5.5e-09)
4338	uC-zmflb73296f01b2.f2	hsf_dna-bind(HMM:7.5e-41)
4339	LIB3075-044-Q1-K1-D2.f2	hsf_dna-bind(HMM:8.1e-09)
4340	rvl700455831.h1.f2	hsf_dna-bind(HMM:8.6e-05)
4341	gct701180355.h1.f3	iaa(HMM:0.00029)
4342	366795_1.R1011.f4	iaa(HMM:0.00031)
4343	44453_2.R1011.f2	iaa(HMM:0.00032)
4344	42794_1.R1011.f3	iaa(HMM:0.00071)
4345	uC-zmflmo17165a04b1.f2	iaa(HMM:0.00097)
4346	clt700042216.f1.f1	iaa(HMM:0.0013)
4347	287224_1.R1011.f2	iaa(HMM:0.0019)
4348	zuv700352703.h1.f1	iaa(HMM:0.0019)
4349	60067_2.R1011.f3	iaa(HMM:0.002)
4350	LIB3279-055-P1-K1-A1.f2	iaa(HMM:0.0021)
4351	LIB3067-052-Q1-K1-G7.f1	iaa(HMM:0.0022)
4352	uC-zmflb73301e09a1.f4	iaa(HMM:0.0023)
4353	uC-zmroteosinte076h10b2.f1	iaa(HMM:0.0025)
4354	90938_2.R1011.f2	iaa(HMM:0.0042)
4355	uC-zmroteosinte058a11b2.f1	iaa(HMM:0.0046)
4356	27519_1.R1011.f4	iaa(HMM:0.0048)
4357	pwr700450469.h1.f3	iaa(HMM:0.0048)
4358	uC-zmromo17026d01a1.f5	iaa(HMM:0.0073)
4359	qmh700029447.f1.f2	iaa(HMM:0.0079)
4360	89902_1.R1011.f3	iaa(HMM:0.0086)
4361	dyk700102340.h1.f3	iaa(HMM:0.014)
4362	273602_2.R1011.f4	iaa(HMM:0.041)
4363	LIB3062-009-Q1-K1-H9.f3	iaa(HMM:0.048)
4364	LIB3156-001-Q1-K1-D9.f3	iaa(HMM:0.06)
4365	nwy700445770.h1.f2	iaa(HMM:0.067)

4366	xmt700262053.h1.f1	iaa(HMM:0.43)
4367	244457_1.R1011.f3	iaa(HMM:1.1)
4368	18074_1.R1011.f3	iaa(HMM:1.1e-12)
4369	36723_3.R1011.f2	iaa(HMM:1.1e-37)
4370	5206_2.R1011.f2	iaa(HMM:1.1e-42)
4371	LIB3069-032-Q1-K1-B5.f1	iaa(HMM:1.2e-06)
4372	18565_1.R1011.f2	iaa(HMM:1.2e-35)
4373	fdz701161796.h1.f2	iaa(HMM:1.3e-19)
4374	165547_1.R1011.f4	iaa(HMM:1.4)
4375	17862_2.R1011.f2	iaa(HMM:1.4e-40)
4376	10914_1.R1011.f1	iaa(HMM:1.4e-46)
4377	99544_1.R1011.f2	iaa(HMM:1.5e-07)
4378	244546_1.R1011.f3	iaa(HMM:1.5e-43)
4379	wty700172062.h1.f2	iaa(HMM:1.6e-07)
4380	113760_1.R1011.f2	iaa(HMM:1.6e-10)
4381	7217_3.R1011.f2	iaa(HMM:1.8e-25)
4382	43613_3.R1011.f3	iaa(HMM:1.8e-30)
4383	7217_1.R1011.f3	iaa(HMM:1.8e-54)
4384	63348_1.R1011.f4	iaa(HMM:1.9e-40)
4385	g4314535.f6	iaa(HMM:2.3e-05)
4386	118813_1.R1011.f3	iaa(HMM:2.5e-05)
4387	fC-zmfl700903946z1.f6	iaa(HMM:2.7e-34)
4388	uC-zmroteosinte030b06b1.f1	iaa(HMM:2.8e-07)
4389	ceu700433713.h1.f1	iaa(HMM:2.8e-29)
4390	177164_1.R1011.f6	iaa(HMM:3.2)
4391	2478_12.R1011.f2	iaa(HMM:3.4e-06)
4392	LIB3067-004-Q1-K1-H5.f1	iaa(HMM:3.4e-21)
4393	dyk700105172.h1.f3	iaa(HMM:3.4e-35)
4394	4794_1.R1011.f2	iaa(HMM:3.5e-36)
4395	39538_1.R1011.f2	iaa(HMM:3.9e-51)
4396	g4647071.f4	iaa(HMM:3e-18)
4397	4943_1.R1011.f2	iaa(HMM:4.1e-40)
4398	pmx700085101.h1.f2	iaa(HMM:4.7e-06)
4399	36723_1.R1011.f2	iaa(HMM:4.7e-17)
4400	LIB3159-016-Q1-K1-H5.f1	iaa(HMM:4.8e-05)
4401	63348_2.R1011.f5	iaa(HMM:5.1e-07)
4402	207353_1.R1011.f2	iaa(HMM:5.1e-09)
4403	44453_1.R1011.f1	iaa(HMM:5.3e-06)
4404	cat700018068.r1.f2	iaa(HMM:5.4e-13)
4405	fdz701160529.h1.f1	iaa(HMM:5.8e-07)
4406	LIB3115-025-P1-K1-G8.f2	iaa(HMM:5.9e-10)
4407	LIB189-028-Q1-E1-C7.f1	iaa(HMM:5e-06)
4408	36723_2.R1011.f2	iaa(HMM:6.4e-08)
4409	wen700335617.h1.f3	iaa(HMM:6.4e-08)
4410	113854_1.R1011.f1	iaa(HMM:6.6e-66)
4411	LIB3070-011-Q1-N1-B9.f2	iaa(HMM:6.8e-06)
4412	6146_3.R1011.f3	iaa(HMM:7.7e-13)
4413	92613_1.R1011.f1	iaa(HMM:7.8e-34)
4414	138145_2.R1011.f3	iaa(HMM:8.8e-08)
4415	LIB3116-025-P1-K1-C6.f3	iaa(HMM:8.9e-09)
4416	uC-zmflmo17297c12b1.f2	iaa(HMM:9.3e-54)
4417	tfd700572494.h1.f1	iaa(HMM:9.6e-10)
4418	qmh700030191.f1.f3	iaa(HMM:9.8e-07)
4419	yyf700348060.h1.f1	ibr(HMM:0.0005)

4420	268028_1.R1011.f2	ibr(HMM:0.015)
4421	180806_1.R1011.f4	ibr(HMM:0.17)
4422	1610_1.R1011.f1	ibr(HMM:1.2e-11)
4423	121748_1.R1011.f3	ibr(HMM:1e-06)
4424	8414_1.R1011.f3	ibr(HMM:2.8e-16)
4425	47794_1.R1011.f3	ibr(HMM:3.6e-06)
4426	19283_1.R1011.f3	ibr(HMM:6.3e-08)
4427	kem700612163.h1.f2	ibr(HMM:6.3e-20)
4428	uC-zmflB73007c10b1.f3	k-box(HMM:0.00013),srf-tf(HMM:2.8e-32)
4429	uC-zmflmo17321d12b1.f3	k-box(HMM:0.00052)
4430	uC-zmroteosinte117g06b1.f1	k-box(HMM:0.0014)
4431	uC-zmflb73020c05b1.f2	k-box(HMM:0.0017)
4432	LIB3069-044-Q1-K1-B9.f3	k-box(HMM:0.0057),srf-tf(HMM:1.4e-36)
4433	LIB3116-025-P1-K1-B6.f2	k-box(HMM:0.007)
4434	uC-zmflb73148g01b1.f1	k-box(HMM:0.0078)
4435	g4730436.f1	k-box(HMM:0.0081),srf-tf(HMM:4.7e-35)
4436	418_1.R1011.f2	k-box(HMM:0.0092),srf-tf(HMM:1.1e-25)
4437	LIB3068-025-Q1-K1-D7.f1	k-box(HMM:0.83)
4438	LIB3067-047-Q1-K1-C2.f1	k-box(HMM:1.1e-06)
4439	166_1.R1011.f2	k-box(HMM:1.2e-08),srf-tf(HMM:1.9e-29)
4440	CPR6867_700163369_FL.f3	k-box(HMM:1.3e-10)
4441	uC-zmflmo17078c09b1.f2	k-box(HMM:1.3e-23)
4442	166_5.R1011.f3	k-box(HMM:1.4e-06)
4443	uC-zmrob73050c02b1.f6	k-box(HMM:1.6e-05)
4444	122_2.R1011.f2	k-box(HMM:1.6e-22)
4445	uC-zmflb73140b06b1.f2	k-box(HMM:1.7e-13)
4446	113_1.R1011.f3	k-box(HMM:1.7e-42),srf-tf(HMM:7.3e-38)
4447	109_2.R1011.f2	k-box(HMM:1.9e-14)
4448	uC-zmflmo17057c07b1.f3	k-box(HMM:1e-06)
4449	610_2.R1011.f3	k-box(HMM:1e-34),srf-tf(HMM:1e-34)
4450	109_1.R1011.f2	k-box(HMM:2.1e-14),srf-tf(HMM:4e-32)
4451	uC-zmflmo17280a06b1.f2	k-box(HMM:2.3e-07)
4452	949_2.R1011.f1	k-box(HMM:2.4e-38),srf-tf(HMM:1.7e-20)
4453	112_2.R1011.f1	k-box(HMM:2.5e-11)
4454	120_3.R1011.f1	k-box(HMM:2.7e-31)
4455	120_2.R1011.f2	k-box(HMM:2.8e-27)
4456	113_3.R1011.f3	k-box(HMM:2.8e-38),srf-tf(HMM:2.8e-37)
4457	LIB3059-037-Q1-K1-A3.f3	k-box(HMM:3.2e-30)
4458	611_2.R1011.f1	k-box(HMM:3.2e-36),srf-tf(HMM:3e-36)
4459	g5268420.f3	k-box(HMM:3.4e-43),srf-tf(HMM:1.3e-11)
4460	544_1.R1011.f2	k-box(HMM:3.4e-43),srf-tf(HMM:4.3e-38)

4461	38372_1.R1011.f1	k-box(HMM:3.5e-05),srf-tf(HMM:1.6e-29)
4462	611_1.R1011.f1	k-box(HMM:3.5e-38),srf-tf(HMM:1.4e-36)
4463	112_1.R1011.f3	k-box(HMM:3.6e-19),srf-tf(HMM:1.9e-09)
4464	610_1.R1011.f2	k-box(HMM:3.7e-35),srf-tf(HMM:1.4e-35)
4465	124_1.R1011.f1	k-box(HMM:3.8e-10)
4466	113_5.R1011.f3	k-box(HMM:3.9e-40),srf-tf(HMM:1.5e-37)
4467	113_6.R1011.f3	k-box(HMM:3.9e-40),srf-tf(HMM:1.5e-37)
4468	166_4.R1011.f2	k-box(HMM:4.1e-05)
4469	107_1.R1011.f3	k-box(HMM:4.4e-12),srf-tf(HMM:1.4e-29)
4470	125_1.R1011.f3	k-box(HMM:4.7e-33),srf-tf(HMM:4.4e-36)
4471	116_1.R1011.f1	k-box(HMM:5.4e-26),srf-tf(HMM:1e-37)
4472	113_4.R1011.f2	k-box(HMM:5.5e-39),srf-tf(HMM:1.6e-37)
4473	123_1.R1011.f3	k-box(HMM:5.7e-25),srf-tf(HMM:1.9e-35)
4474	119_1.R1011.f3	k-box(HMM:5.8e-08)
4475	4634_1.R1011.f2	k-box(HMM:5.9e-18)
4476	LIB3116-025-P1-K2-B6.f1	k-box(HMM:6.4e-07)
4477	LIB3067-059-Q1-K1-C6.f1	k-box(HMM:6.6e-07),srf-tf(HMM:1.3e-16)
4478	122_1.R1011.f1	k-box(HMM:6.7e-42),srf-tf(HMM:3e-37)
4479	LIB3088-010-Q1-K1-D9.f3	k-box(HMM:7.1e-06)
4480	g939780.f1	k-box(HMM:7.2e-43),srf-tf(HMM:4.9e-37)
4481	uC-zmflb73119c08a1.f3	k-box(HMM:7.5e-06)
4482	120_1.R1011.f1	k-box(HMM:9.3e-06)
4483	949_1.R1011.f1	k-box(HMM:9.3e-37),srf-tf(HMM:3.7e-19)
4484	hbs701183413.h1.f1	krab(HMM:3.6e-05)
4485	LIB148-007-Q1-E1-H9.f2	lim(HMM:0.0007)
4486	LIB3066-032-Q1-K1-B12.f1	lim(HMM:0.001)
4487	211710_1.R1011.f3	lim(HMM:0.0021)
4488	LIB3075-048-Q1-K1-D11.f3	lim(HMM:0.055)
4489	uC-zmroteosinte017b09b1.f3	lim(HMM:0.097)
4490	gct701174937.h1.f2	lim(HMM:0.16)
4491	101_4.R1011.f1	lim(HMM:0.35)
4492	pmx700086732.h1.f1	lim(HMM:0.42)
4493	1647_2.R1011.f1	lim(HMM:1.2e-31)
4494	106476_1.R1011.f1	lim(HMM:1.3e-11)
4495	g3341091.f6	lim(HMM:1.7e-11)
4496	1647_4.R1011.f3	lim(HMM:1.9e-14)
4497	fC-zmle700870883a1.f2	lim(HMM:1.9e-14)
4498	uC-zmflmo17303c04b1.f2	lim(HMM:1e-21)
4499	1647_3.R1011.f1	lim(HMM:2.2e-14)

4500	1647_1.R1011.f1	lim(HMM:2.2e-32)
4501	wyr700235386.h1.f2	lim(HMM:3.1e-06)
4502	xsy700208410.h1.f1	lim(HMM:3.9e-12)
4503	uC-zmflmo17169d03a1.f3	lim(HMM:3.9e-22)
4504	fdz701158756.h1.f1	lim(HMM:4.4e-09)
4505	pwr700450670.h1.f1	lim(HMM:4.7e-10)
4506	94503_1.R1011.f3	lim(HMM:4.9e-14)
4507	101_2.R1011.f3	lim(HMM:4e-14)
4508	hbs701182729.h1.f4	lim(HMM:5.2e-06)
4509	101_1.R1011.f3	lim(HMM:8.3e-33)
4510	83525_1.R1011.f2	lim(HMM:8e-32)
4511	756_8.R1011.f1	linker_histone(HMM:0.00018)
4512	LIB3137-001-Q1-K1-A5.f1	linker_histone(HMM:0.00022)
4513	uC-zmflb73178a11b1.f1	linker_histone(HMM:0.00047)
4514	756_3.R1011.f3	linker_histone(HMM:0.00052)
4515	LIB3150-101-P1-N1-A3.f1	linker_histone(HMM:0.0076)
4516	LIB3076-019-Q1-K1-B5.f3	linker_histone(HMM:0.0096)
4517	uC-zmflmo17069f02b1.f1	linker_histone(HMM:0.36)
4518	g4585618.f1	linker_histone(HMM:1.1e-22)
4519	666_2.R1011.f5	linker_histone(HMM:1.5e-30)
4520	uC-zmflmo17308b11b1.f1	linker_histone(HMM:1.6e-05)
4521	LIB3069-035-Q1-K1-A11.f2	linker_histone(HMM:1.9e-10)
4522	g5268367.f1	linker_histone(HMM:1.9e-23)
4523	14297_1.R1011.f1	linker_histone(HMM:1.9e-34)
4524	4905_2.R1011.f1	linker_histone(HMM:1e-24)
4525	180_1.R1011.f2	linker_histone(HMM:2.7e-07),myb_dna-binding(HMM:6.5e-05)
4526	rvt700550793.h1.f3	linker_histone(HMM:2.9)
4527	756_4.R1011.f2	linker_histone(HMM:3.4e-33)
4528	19893_2.R1011.f1	linker_histone(HMM:4.3e-05)
4529	LIB3076-020-Q1-K1-B1.f3	linker_histone(HMM:4e-07)
4530	19893_1.R1011.f1	linker_histone(HMM:5.5e-22)
4531	4905_1.R1011.f1	linker_histone(HMM:5e-33)
4532	14369_1.R1011.f3	linker_histone(HMM:8.1e-10),myb_dna-binding(HMM:2.1e-05)
4533	LIB3067-044-Q1-K1-F9.f2	linker_histone(HMM:8.4)
4534	uC-zmflmo17153e05b1.f1	linker_histone(HMM:8.6)
4535	756_1.R1011.f1	linker_histone(HMM:9.6e-35)
4536	108800_1.R1011.f2	linker_histone(HMM:9.7e-13)
4537	tzu700203222.h1.f3	myb_dna-binding(HMM:0.00013)
4538	1086_2.R1011.f3	myb_dna-binding(HMM:0.0002)
4539	92085_1.R1011.f1	myb_dna-binding(HMM:0.00023)
4540	119067_1.R1011.f2	myb_dna-binding(HMM:0.00025)
4541	235108_1.R1011.f3	myb_dna-binding(HMM:0.00026)
4542	6030_1.R1011.f1	myb_dna-binding(HMM:0.00049)
4543	uwc700151452.h1.f2	myb_dna-binding(HMM:0.00086)

4544	47690_1.R1011.f3	myb_dna-binding(HMM:0.00096)
4545	g3157223.f1	myb_dna-binding(HMM:0.001)
4546	129899_1.R1011.f1	myb_dna-binding(HMM:0.0012)
4547	9893_3.R1011.f1	myb_dna-binding(HMM:0.0019)
4548	uC-zmflb73085c02b2.f1	myb_dna-binding(HMM:0.0021)
4549	242350_1.R1011.f2	myb_dna-binding(HMM:0.0024)
4550	965_13.R1011.f1	myb_dna-binding(HMM:0.0025)
4551	uC-zmrob73057g12a1.f1	myb_dna-binding(HMM:0.0026)
4552	141721_1.R1011.f1	myb_dna-binding(HMM:0.0027)
4553	111722_1.R1011.f3	myb_dna-binding(HMM:0.003)
4554	wty700167056.h1.f1	myb_dna-binding(HMM:0.0063)
4555	13671_1.R1011.f1	myb_dna-binding(HMM:0.013)
4556	ymt700219745.h1.f2	myb_dna-binding(HMM:0.015)
4557	100888_1.R1011.f1	myb_dna-binding(HMM:0.034)
4558	LIB3150-093-P1-N1-A8.f2	myb_dna-binding(HMM:0.059)
4559	56162_2.R1011.f1	myb_dna-binding(HMM:0.067)
4560	rvt700550259.h1.f2	myb_dna-binding(HMM:0.087)
4561	3037_1.R1011.f3	myb_dna-binding(HMM:0.1)
4562	wty700170367.h1.f1	myb_dna-binding(HMM:0.11)
4563	62090_2.R1011.f3	myb_dna-binding(HMM:0.13)
4564	9893_2.R1011.f3	myb_dna-binding(HMM:0.14)
4565	ypc700805836.h1.f6	myb_dna-binding(HMM:0.18)
4566	1124_5.R1011.f5	myb_dna-binding(HMM:0.27)
4567	fxb700397574.h1.f2	myb_dna-binding(HMM:0.43)
4568	uC-zmflmo17344c12b1.f3	myb_dna-binding(HMM:0.44)
4569	1124_3.R1011.f6	myb_dna-binding(HMM:1.1e-10)
4570	LIB3079-030-Q1-K1-F3.f2	myb_dna-binding(HMM:1.1e-10)
4571	tzu700203377.h1.f1	myb_dna-binding(HMM:1.2e-21)
4572	18719_1.R1011.f3	myb_dna-binding(HMM:1.3e-10)
4573	18719_2.R1011.f2	myb_dna-binding(HMM:1.3e-10)
4574	ceu700422519.h1.f2	myb_dna-binding(HMM:1.4e-16)
4575	uer700577328.h1.f2	myb_dna-binding(HMM:1.4e-17)
4576	86820_1.R1011.f1	myb_dna-binding(HMM:1.4e-21)
4577	g1491932.f2	myb_dna-binding(HMM:1.4e-45)
4578	g168589.f2	myb_dna-binding(HMM:1.4e-45)
4579	196036_1.R1011.f1	myb_dna-binding(HMM:1.5e-08)
4580	49266_1.R1011.f3	myb_dna-binding(HMM:1.5e-16)
4581	134451_1.R1011.f1	myb_dna-binding(HMM:1.6e-10)
4582	LIB3151-057-Q1-K1-E8.f3	myb_dna-binding(HMM:1.6e-20)
4583	g168591.f2	myb_dna-binding(HMM:1.7e-22)
4584	965_23.R1011.f1	myb_dna-binding(HMM:1.7e-42)
4585	14894_1.R1011.f2	myb_dna-binding(HMM:1.8e-40)
4586	81644_2.R1011.f2	myb_dna-binding(HMM:1.9e-05)
4587	35267_2.R1011.f1	myb_dna-binding(HMM:1.9e-06)
4588	gct701176532.h1.f1	myb_dna-binding(HMM:1.9e-11)
4589	uC-zmroB73017f11b1.f1	myb_dna-binding(HMM:1.9e-11)
4590	71261_1.R1011.f1	myb_dna-binding(HMM:1.9e-37)
4591	uC-zmflb73162h04b2.f3	myb_dna-binding(HMM:1e-07)
4592	116851_1.R1011.f3	myb_dna-binding(HMM:2.1e-10)
4593	uC-zmrob73076b09b1.f2	myb_dna-binding(HMM:2.1e-12)
4594	43747_1.R1011.f1	myb_dna-binding(HMM:2.1e-35)
4595	11369_2.R1011.f1	myb_dna-binding(HMM:2.2e-07)
4596	LIB3180-030-P2-M2-G3.f3	myb_dna-binding(HMM:2.2e-07)

4597	8195_2.R1011.f2	myb_dna-binding(HMM:2.3e-09)
4598	uC-zmflmo17394f11a1.f1	myb_dna-binding(HMM:2.4e-27)
4599	35267_1.R1011.f1	myb_dna-binding(HMM:2.4e-39)
4600	37039_3.R1011.f2	myb_dna-binding(HMM:2.4e-44)
4601	1086_1.R1011.f1	myb_dna-binding(HMM:2.5e-24)
4602	uC-zmflb73143e02b1.f2	myb_dna-binding(HMM:2.5e-42)
4603	211273_1.R1011.f3	myb_dna-binding(HMM:2.6e-06)
4604	360_1.R1011.f5	myb_dna-binding(HMM:2.6e-11)
4605	ypc700802849.h1.f1	myb_dna-binding(HMM:2.6e-20)
4606	wyr700237918.h1.f3	myb_dna-binding(HMM:2.7e-06)
4607	wyr700243864.h1.f2	myb_dna-binding(HMM:2.8e-05)
4608	LIB3078-013-Q1-K1-H9.f2	myb_dna-binding(HMM:2.8e-11)
4609	14894_3.R1011.f3	myb_dna-binding(HMM:2.9e-41)
4610	1334_1.R1011.f3	myb_dna-binding(HMM:3.4)
4611	qmh700027865.f1.f2	myb_dna-binding(HMM:3.7e-05)
4612	tzu700204208.h1.f1	myb_dna-binding(HMM:3.7e-14)
4613	92525_1.R1011.f3	myb_dna-binding(HMM:3e-45)
4614	wty700171752.h1.f2	myb_dna-binding(HMM:4.1e-07)
4615	14894_2.R1011.f2	myb_dna-binding(HMM:4.1e-39)
4616	9893_4.R1011.f3	myb_dna-binding(HMM:4.4)
4617	46504_1.R1011.f2	myb_dna-binding(HMM:4.5e-08),zz(HMM:1.2e-11)
4618	uC-zmrob73011a04b1.f2	myb_dna-binding(HMM:4.5e-15)
4619	120679_1.R1011.f1	myb_dna-binding(HMM:4.7e-37)
4620	uC-zmflmo17176a01b1.f2	myb_dna-binding(HMM:4.8e-19)
4621	uC-zmflb73017a03b1.f3	myb_dna-binding(HMM:4.8e-21)
4622	8195_3.R1011.f1	myb_dna-binding(HMM:4.9e-10)
4623	136974_1.R1011.f2	myb_dna-binding(HMM:4e-09)
4624	g5268844.f2	myb_dna-binding(HMM:4e-41)
4625	224582_1.R1011.f3	myb_dna-binding(HMM:5.4e-23)
4626	278384_1.R1011.f3	myb_dna-binding(HMM:5.6e-19)
4627	44418_2.R1011.f2	myb_dna-binding(HMM:5.8e-06)
4628	vux700159730.h1.f2	myb_dna-binding(HMM:5.9e-10)
4629	133302_1.R1011.f3	myb_dna-binding(HMM:5.9e-41)
4630	uC-zmflmo17173b11b1.f3	myb_dna-binding(HMM:5e-11)
4631	65645_1.R1011.f2	myb_dna-binding(HMM:6.4e-40)
4632	180_3.R1011.f3	myb_dna-binding(HMM:6.5e-05)
4633	3753_1.R1011.f2	myb_dna-binding(HMM:6.6e-05)
4634	3005_5.R1011.f3	myb_dna-binding(HMM:6.6e-16)
4635	pwr700450354.h1.f3	myb_dna-binding(HMM:6.6e-20)
4636	uC-zmflmo17052e02b1.f2	myb_dna-binding(HMM:6e-25)
4637	LIB84-023-Q1-E1-D6.f2	myb_dna-binding(HMM:7.4e-12)
4638	224186_1.R1011.f1	myb_dna-binding(HMM:7.5e-09)
4639	uC-zmflB73025b03b2.f3	myb_dna-binding(HMM:7.5e-35)
4640	111964_1.R1011.f2	myb_dna-binding(HMM:7.6e-39)
4641	354078_1.R1011.f2	myb_dna-binding(HMM:7.8e-09)
4642	uC-zmflb73234b10b2.f3	myb_dna-binding(HMM:8.1e-13)
4643	LIB189-026-Q1-E1-F3.f1	myb_dna-binding(HMM:8.2e-22)
4644	81644_1.R1011.f1	myb_dna-binding(HMM:8.6e-20)
4645	63048_1.R1011.f2	myb_dna-binding(HMM:8.7e-11)
4646	qmh700026342.f1.f2	myb_dna-binding(HMM:8.9e-21)
4647	9893_1.R1011.f3	myb_dna-binding(HMM:9.1e-15)
4648	37039_2.R1011.f2	myb_dna-binding(HMM:9.3e-45)
4649	xsy700211270.h1.f2	myb_dna-binding(HMM:9.4e-20)

4650	fC-zmro700835640f1.f3	myb_dna-binding(HMM:9.9)
4651	pwr700451947.h1.f3	myc_n_term(HMM:1.3e-07)
4652	LIB3062-027-Q1-K1-G5.f3	nam(HMM:0.00016)
4653	wyr700240279.h1.f2	nam(HMM:0.00045)
4654	108682_1.R1011.f1	nam(HMM:0.00048)
4655	tfd700574820.h1.f2	nam(HMM:0.0008)
4656	LIB3060-045-Q1-K1-G6.f3	nam(HMM:0.0013)
4657	xsy700208075.h1.f3	nam(HMM:0.0013)
4658	LIB3060-022-Q1-K1-C4.f3	nam(HMM:0.0027)
4659	95404_1.R1011.f4	nam(HMM:0.0029)
4660	54370_1.R1011.f1	nam(HMM:0.0038)
4661	45380_1.R1011.f1	nam(HMM:0.0041)
4662	LIB3060-029-Q1-K1-C8.f3	nam(HMM:0.01)
4663	134883_1.R1011.f1	nam(HMM:0.027)
4664	201218_1.R1011.f1	nam(HMM:0.052)
4665	LIB3117-005-Q1-K1-A2.f2	nam(HMM:0.2)
4666	wyr700235447.h1.f2	nam(HMM:0.22)
4667	LIB3137-041-Q1-K1-C9.f3	nam(HMM:0.27)
4668	206869_1.R1011.f1	nam(HMM:0.72)
4669	301_1.R1011.f4	nam(HMM:1.1e-06)
4670	uC-zmrob73057e10a1.f1	nam(HMM:1.1e-06)
4671	73768_1.R1011.f3	nam(HMM:1.1e-48)
4672	124375_1.R1011.f3	nam(HMM:1.1e-71)
4673	wyr700243269.h1.f2	nam(HMM:1.2)
4674	LIB3088-025-Q1-K1-E9.f2	nam(HMM:1.2e-06)
4675	LIB3069-033-Q1-K1-B10.f2	nam(HMM:1.4)
4676	LIB3151-016-Q1-K1-D2.f3	nam(HMM:1.4e-15)
4677	19925_2.R1011.f1	nam(HMM:1.4e-80)
4678	242069_1.R1011.f1	nam(HMM:1.5e-18)
4679	215216_1.R1011.f1	nam(HMM:1.6e-12)
4680	202414_1.R1011.f3	nam(HMM:1.7e-36)
4681	uwc700150130.h1.f3	nam(HMM:1e-10)
4682	uC-zmflmo17132d12b1.f2	nam(HMM:2.1)
4683	10371_3.R1011.f3	nam(HMM:2.1e-22)
4684	46032_4.R1011.f2	nam(HMM:2.3)
4685	cyk700051638.f1.f1	nam(HMM:2.3e-13)
4686	ymt700219252.h1.f1	nam(HMM:2.5e-13)
4687	qmh700028170.f1.f3	nam(HMM:2.6e-08)
4688	vux700157267.h1.f2	nam(HMM:2.6e-08)
4689	24806_3.R1011.f4	nam(HMM:2.7e-83)
4690	12221_1.R1011.f1	nam(HMM:2.8e-41)
4691	24806_2.R1011.f5	nam(HMM:2.8e-67)
4692	dyk700102188.h1.f2	nam(HMM:2.9)
4693	uwc700149818.h1.f1	nam(HMM:3.1e-11)
4694	970_6.R1011.f2	nam(HMM:3.1e-37)
4695	g5555593.f3	nam(HMM:3.2e-64)
4696	30619_1.R1011.f2	nam(HMM:3.3e-79)
4697	207681_1.R1011.f2	nam(HMM:3.5)
4698	uC-zmflmo17160c10b1.f3	nam(HMM:3.5e-09)
4699	uC-zmflmo17336e02b1.f1	nam(HMM:3.7)
4700	LIB3115-029-P1-K1-F7.f2	nam(HMM:3.7e-16)
4701	LIB3136-019-Q1-K1-C9.f2	nam(HMM:3.8e-05)
4702	371645_1.R1011.f4	nam(HMM:4.5e-08)
4703	120771_1.R1011.f1	nam(HMM:4.5e-36)

4704	ymt700221866.h1.f1	nam(HMM:4.6e-10)
4705	uC-zmrob73050h05b1.f1	nam(HMM:4.8e-75)
4706	24806_1.R1011.f5	nam(HMM:4.8e-80)
4707	uC-zmrob73012a06b1.f1	nam(HMM:4e-22)
4708	219835_1.R1011.f1	nam(HMM:5.1e-09)
4709	LIB3182-009-P2-M1-B4.f1	nam(HMM:5.2e-07)
4710	2917_1.R1011.f3	nam(HMM:5.3)
4711	LIB3116-004-Q1-K2-F7.f1	nam(HMM:5.7e-08)
4712	qmh700029568.f1.f2	nam(HMM:5.8)
4713	115174_1.R1011.f3	nam(HMM:5.8e-34)
4714	LIB3182-016-P2-M1-F1.f2	nam(HMM:6.1e-06)
4715	LIB3066-040-Q1-K1-A5.f2	nam(HMM:6.2e-05)
4716	wyr700239811.h1.f2	nam(HMM:6.2e-06)
4717	205197_2.R1011.f3	nam(HMM:6.3e-11)
4718	tzu700201601.h1.f2	nam(HMM:6.8)
4719	hbs701182246.h1.f1	nam(HMM:6.8e-05)
4720	121716_1.R1011.f2	nam(HMM:6.9e-06)
4721	xmt700265206.h1.f2	nam(HMM:6.9e-39)
4722	10371_1.R1011.f1	nam(HMM:6.9e-77)
4723	LIB3150-079-P1-N1-E4.f3	nam(HMM:7.7e-16)
4724	LIB3076-012-Q1-K1-F12.f2	nam(HMM:8.1e-08)
4725	205197_1.R1011.f3	nam(HMM:8.3e-14)
4726	uC-zmflb73083h12b2.f1	nam(HMM:8.4e-08)
4727	uC-zmflmo170114g01b1.f3	nam(HMM:8.4e-37)
4728	970_5.R1011.f3	nam(HMM:8.5e-43)
4729	LIB3151-013-Q1-K1-H9.f3	nam(HMM:9.3e-32)
4730	uC-zmflb73187e11b1.f1	nam(HMM:9.7e-13)
4731	163322_1.R1011.f3	nam(HMM:9.9e-10)
4732	wty700168653.h1.f3	nam(HMM:9e-06)
4733	uC-zmflmo17283a03b1.f1	nam(HMM:9e-09)
4734	7647_3.R1011.f3	nap_family(HMM:0.0004)
4735	LIB3059-023-Q1-K1-G2.f2	nap_family(HMM:0.0027)
4736	LIB3150-108-P2-K1-C6.f6	nap_family(HMM:0.004)
4737	15810_1.R1011.f3	nap_family(HMM:1.3e-09)
4738	6060_1.R1011.f1	nap_family(HMM:1.5e-13)
4739	7647_1.R1011.f2	nap_family(HMM:1.5e-28)
4740	LIB3150-004-Q1-N1-D4.f3	nap_family(HMM:1.7e-09)
4741	21318_1.R1011.f1	nap_family(HMM:2.3e-136)
4742	7647_2.R1011.f3	nap_family(HMM:3.7e-11)
4743	LIB3062-040-Q1-K1-G7.f3	nap_family(HMM:6.7e-16)
4744	g4885774.f6	nap_family(HMM:6e-10)
4745	xyt700343958.h1.f2	nap_family(HMM:9.8e-09)
4746	rvt700552474.h1.f4	nap_family(HMM:9e-14)
4747	71771_1.R1011.f2	nap_family(HMM:9e-29)
4748	tzu700201204.h1.f3	phd(HMM:0.00027)
4749	19796_2.R1011.f1	phd(HMM:0.00028)
4750	18004_1.R1011.f2	phd(HMM:0.00053)
4751	uC-zmflb73180d03b1.f1	phd(HMM:0.00077),zf-c3hc4(HMM:0.0007)
4752	32_1.R1011.f1	phd(HMM:0.0026)
4753	113229_1.R1011.f3	phd(HMM:0.0042)
4754	111362_1.R1011.f1	phd(HMM:0.0056)
4755	65252_1.R1011.f1	phd(HMM:0.0062)
4756	839_9.R1011.f1	phd(HMM:0.0072)

4757	sem700930118.h1.f3	phd(HMM:0.0072)
4758	133965_1.R1011.f1	phd(HMM:0.01)
4759	35755_1.R1011.f3	phd(HMM:0.045)
4760	227366_1.R1011.f2	phd(HMM:0.11)
4761	39_1.R1011.f2	phd(HMM:0.11)
4762	LIB3076-004-Q1-K1-D10.f2	phd(HMM:0.11)
4763	161337_1.R1011.f3	phd(HMM:0.12)
4764	24_1.R1011.f2	phd(HMM:0.13)
4765	96044_1.R1011.f3	phd(HMM:0.15)
4766	133844_1.R1011.f3	phd(HMM:0.16),zf-c3hc4(HMM:2.1e-08)
4767	g5006147.f6	phd(HMM:0.18)
4768	g511367.f3	phd(HMM:0.29)
4769	uC-zmflb73232a09b1.f3	phd(HMM:0.49)
4770	rvt700549516.h1.f1	phd(HMM:1.1e-09)
4771	g4938805.f5	phd(HMM:1.2e-05)
4772	5182_2.R1011.f3	phd(HMM:1.2e-10)
4773	33917_1.R1011.f1	phd(HMM:1.2e-11)
4774	18361_3.R1011.f1	phd(HMM:1.4e-12)
4775	LIB3059-004-Q1-K1-G10.f1	phd(HMM:1.5e-05)
4776	18361_6.R1011.f1	phd(HMM:1.5e-12)
4777	LIB3079-026-Q1-K1-C12.f6	phd(HMM:1.5e-13)
4778	33_1.R1011.f3	phd(HMM:1.7e-26)
4779	33_2.R1011.f2	phd(HMM:1.8e-06)
4780	37_1.R1011.f1	phd(HMM:2.1e-17)
4781	33917_2.R1011.f2	phd(HMM:2.2e-11)
4782	170811_1.R1011.f4	phd(HMM:2.4e-11)
4783	31_1.R1011.f1	phd(HMM:2.7e-10)
4784	80836_1.R1011.f2	phd(HMM:2.9e-06)
4785	85816_1.R1011.f2	phd(HMM:3.1)
4786	149233_1.R1011.f2	phd(HMM:3.3e-11)
4787	2345_1.R1011.f1	phd(HMM:3.4e-12)
4788	34_1.R1011.f1	phd(HMM:3.9e-10)
4789	12886_1.R1011.f2	phd(HMM:4.6e-11),zf-c3hc4(HMM:0.11)
4790	65563_1.R1011.f2	phd(HMM:4e-06)
4791	4863_1.R1011.f3	phd(HMM:4e-11)
4792	53455_1.R1011.f1	phd(HMM:5.6e-12)
4793	19796_1.R1011.f2	phd(HMM:6.9e-11)
4794	5182_1.R1011.f2	phd(HMM:7.9e-11)
4795	ypc700806368.h1.f3	response_reg(HMM:0.00012)
4796	65085_2.R1011.f1	response_reg(HMM:0.00013)
4797	LIB3180-050-P2-M1-A9.f1	response_reg(HMM:0.00014)
4798	uC-zmflmo17226h04a1.f6	response_reg(HMM:0.00041)
4799	uC-zmrob73055d04b1.f3	response_reg(HMM:0.0014)
4800	130_2.R1011.f3	response_reg(HMM:0.0032)
4801	ymt700223944.h1.f3	response_reg(HMM:0.0039)
4802	LIB3079-004-Q1-K1-A2.f2	response_reg(HMM:0.0064)
4803	xjt700094034.h1.f3	response_reg(HMM:0.0081)
4804	LIB3079-022-Q1-K1-C1.f3	response_reg(HMM:1.1e-05)
4805	337940_1.R1011.f3	response_reg(HMM:1.2e-14)
4806	92601_1.R1011.f2	response_reg(HMM:1.3e-31)
4807	451_2.R1011.f3	response_reg(HMM:1.4e-28)
4808	uC-zmflmo17122e02b1.f1	response_reg(HMM:1.6e-06)

4809	uC-zmflb73145a08b1.f6	response_reg(HMM:1.7e-23)
4810	16902_1.R1011.f2	response_reg(HMM:1.7e-27)
4811	127220_1.R1011.f3	response_reg(HMM:1.9e-25)
4812	40825_1.R1011.f1	response_reg(HMM:1e-21)
4813	39702_1.R1011.f2	response_reg(HMM:2.1e-33)
4814	93258_1.R1011.f1	response_reg(HMM:2.7e-15)
4815	130_1.R1011.f3	response_reg(HMM:2e-24)
4816	85312_1.R1011.f2	response_reg(HMM:3.1e-31)
4817	262612_1.R1011.f1	response_reg(HMM:3.3)
4818	uC-zmflmo17228b09a1.f2	response_reg(HMM:3.3e-33)
4819	uC-zmflmo17d08b1.f1	response_reg(HMM:3.6e-11)
4820	3176_1.R1011.f1	response_reg(HMM:3.7e-28)
4821	uC-zmflb73267e04b2.f2	response_reg(HMM:3e-05)
4822	33496_1.R1011.f2	response_reg(HMM:4.1e-11)
4823	83822_1.R1011.f1	response_reg(HMM:4.3e-07)
4824	121995_1.R1011.f2	response_reg(HMM:4.3e-10)
4825	451_1.R1011.f1	response_reg(HMM:5.4e-31)
4826	5057_2.R1011.f2	response_reg(HMM:5.7e-29)
4827	uC-zmflmo17225f10a1.f3	response_reg(HMM:6.2e-19)
4828	uC-zmflmo17252b11a1.f1	response_reg(HMM:6.6e-21)
4829	89322_1.R1011.f1	response_reg(HMM:6.7e-12)
4830	uC-zmflmo17169d11a1.f2	response_reg(HMM:7.2e-05)
4831	36385_1.R1011.f1	response_reg(HMM:7.9e-11)
4832	LIB3059-026-Q1-K1-H6.f1	response_reg(HMM:8.9e-05)
4833	5057_1.R1011.f3	response_reg(HMM:9.1e-30)
4834	LIB3069-024-Q1-K1-G9.f2	runt(HMM:0.008)
4835	LIB3136-001-P1-K1-D6.f2	sbpb(HMM:0.00086)
4836	uC-zmflb73276d09b1.f3	sbpb(HMM:0.0046)
4837	pmx700084920.h1.f1	sbpb(HMM:1.3e-10)
4838	cat700019575.r1.f3	sbpb(HMM:1.4e-13)
4839	uwc700150553.h1.f3	sbpb(HMM:1.4e-39)
4840	qmh700030362.f1.f3	sbpb(HMM:1.7e-10)
4841	67995_1.R1011.f3	sbpb(HMM:1.8e-34)
4842	62560_1.R1011.f2	sbpb(HMM:2.2e-05)
4843	235145_1.R1011.f1	sbpb(HMM:2.4e-15)
4844	uC-zmflb73113c09a2.f4	sbpb(HMM:3.3e-18)
4845	241_44.R1011.f6	sbpb(HMM:4.5e-39)
4846	1173_1.R1011.f3	sbpb(HMM:4.6e-44)
4847	LIB3069-037-Q1-K1-C4.f1	sbpb(HMM:5.8e-10)
4848	xyt700343163.h1.f2	sbpb(HMM:5.8e-16)
4849	uC-zmflb73372c09a1.f6	sbpb(HMM:8.1)
4850	afb700381372.h1.f2	scan(HMM:2.2e-09)
4851	LIB3116-007-Q1-K1-E8.f1	scr(HMM:0.00088)
4852	cyk700051838.f1.f1	scr(HMM:0.0022)
4853	LIB3136-038-P1-K1-F6.f3	scr(HMM:0.0036)
4854	uC-zmflmo17275c01a1.f5	scr(HMM:0.005)
4855	uC-zmroteosinte016b06b1.f3	scr(HMM:0.006)
4856	218432_1.R1011.f3	scr(HMM:0.0084)
4857	55105_1.R1011.f1	scr(HMM:0.0085)
4858	240174_1.R1011.f3	scr(HMM:0.029)
4859	2021_9.R1011.f1	scr(HMM:1.3)
4860	mwy700442142.h1.f1	scr(HMM:1.3e-05)
4861	31248_1.R1011.f2	scr(HMM:1.4e-27)
4862	86173_1.R1011.f1	scr(HMM:1.6e-37)

4863	LIB3279-008-P1-K1-A1.f3	scr(HMM:1.7e-05)
4864	70371_1.R1011.f3	scr(HMM:1.7e-14)
4865	85163_1.R1011.f3	scr(HMM:1.9e-13)
4866	1042_1.R1011.f1	scr(HMM:1.9e-16)
4867	6174_1.R1011.f3	scr(HMM:2.1e-27)
4868	g4152171.f3	scr(HMM:2.3)
4869	LIB3069-022-Q1-K1-E10.f2	scr(HMM:2.3e-22)
4870	kem700612202.h1.f3	scr(HMM:2.3e-24)
4871	LIB83-013-Q1-E1-F6.f2	scr(HMM:2.4e-06)
4872	645_2.R1011.f4	scr(HMM:2.5e-68)
4873	35597_1.R1011.f2	scr(HMM:2.8e-05)
4874	LIB148-030-Q1-E1-E4.f4	scr(HMM:2.9e-30)
4875	gct701173786.h1.f2	scr(HMM:3.8e-12)
4876	uC-zmflb73073f08b3.f5	scr(HMM:4.2e-10)
4877	uC-zmflMo17064f12b1.f3	scr(HMM:4.3e-10)
4878	33292_1.R1011.f3	scr(HMM:4.8e-114)
4879	uC-zmroB73014d08b1.f3	scr(HMM:5.3e-06)
4880	19366_1.R1011.f2	scr(HMM:5.3e-20)
4881	LIB3076-032-Q1-K1-C4.f1	scr(HMM:5.7e-14)
4882	19366_2.R1011.f3	scr(HMM:6.5e-07)
4883	39453_1.R1011.f1	scr(HMM:6.8e-06)
4884	177209_1.R1011.f5	scr(HMM:7.2e-19)
4885	2021_4.R1011.f2	scr(HMM:7.2e-20)
4886	fdz701163921.h1.f1	scr(HMM:7.4e-09)
4887	uC-zmflb73033d10b1.f3	scr(HMM:7.4e-15)
4888	91255_1.R1011.f3	scr(HMM:7.5e-07)
4889	44990_1.R1011.f1	scr(HMM:7.7e-12)
4890	101733_1.R1011.f3	scr(HMM:8.8e-17)
4891	xsy700212015.h1.f3	scr(HMM:8.8e-32)
4892	uC-zmflmo17289a06b1.f1	scr(HMM:9.3e-05)
4893	72518_1.R1011.f1	scr(HMM:9.3e-12)
4894	wyr700237065.h1.f3	scr(HMM:9.7e-06)
4895	ntr700074722.h1.f1	scr(HMM:9.9e-28)
4896	ceu700432452.h1.f3	set(HMM:0.00016)
4897	nwy700445574.h1.f2	set(HMM:0.0002)
4898	159774_1.R1011.f6	set(HMM:0.00046)
4899	159774_2.R1011.f4	set(HMM:0.00059)
4900	yne700378914.h1.f2	set(HMM:0.00059)
4901	LIB3075-019-Q1-K1-E9.f2	set(HMM:0.00076)
4902	uC-zmflb73150d09b1.f1	set(HMM:0.0012)
4903	LIB3116-015-P1-K1-H1.f1	set(HMM:0.0015)
4904	4642_1.R1011.f1	set(HMM:0.07)
4905	112014_1.R1011.f3	set(HMM:0.12)
4906	201970_1.R1011.f2	set(HMM:0.14)
4907	82277_1.R1011.f2	set(HMM:0.85)
4908	xjt700096952.h1.f1	set(HMM:1.1e-11)
4909	uC-zmflb731230c05a1.f6	set(HMM:1.1e-12)
4910	1755_1.R1011.f2	set(HMM:1.1e-36)
4911	54645_1.R1011.f2	set(HMM:1.1e-46)
4912	uC-zmflb73230c10b2.f1	set(HMM:1.3e-06)
4913	LIB3079-056-Q1-K1-E1.f1	set(HMM:1.5e-15)
4914	LIB3075-013-Q1-K1-F1.f1	set(HMM:1.6e-12)
4915	70655_1.R1011.f3	set(HMM:1.6e-26)
4916	afb700381224.h1.f1	set(HMM:1.7e-06)

4917	gct701180481.h1.f3	set(HMM:1.7e-13)
4918	uC-zmflb73139a02b1.f1	set(HMM:1.8e-05)
4919	4193_1.R1011.f3	set(HMM:1.8e-50)
4920	138441_1.R1011.f2	set(HMM:1.9e-14)
4921	8673_1.R1011.f3	set(HMM:2.6e-05)
4922	211176_1.R1011.f2	set(HMM:2.7)
4923	5363_1.R1011.f1	set(HMM:3.1e-26)
4924	LIB3062-051-Q1-K1-A12.f1	set(HMM:3.2)
4925	5332_1.R1011.f1	set(HMM:3.3e-34)
4926	78685_1.R1011.f1	set(HMM:4e-06)
4927	LIB3150-023-Q1-N1-F1.f3	set(HMM:4e-11)
4928	uC-zmroteosinte008f10b1.f3	set(HMM:5.3e-53)
4929	140423_1.R1011.f2	set(HMM:5.4e-55)
4930	cjh700196512.h1.f2	set(HMM:6.4e-14)
4931	42686_1.R1011.f1	set(HMM:7.8e-44)
4932	fdz701160861.h1.f1	set(HMM:8.2e-08)
4933	107223_1.R1011.f2	set(HMM:9.5e-19)
4934	18141_1.R1011.f1	set(HMM:9.7e-07)
4935	rvl700456152.h1.f3	set(HMM:9.9e-13)
4936	LIB3067-013-Q1-K1-F4.f3	snf2_n(HMM:0.00016),zf-c3hc4(HMM:0.18)
4937	104440_1.R1011.f2	snf2_n(HMM:0.006)
4938	nbm700468170.h1.f2	snf2_n(HMM:0.083)
4939	LIB3066-024-Q1-K1-F6.f2	snf2_n(HMM:0.75)
4940	85215_1.R1011.f1	snf2_n(HMM:0.78)
4941	96331_1.R1011.f3	snf2_n(HMM:1.1e-45)
4942	uC-zmflmo17223c09b1.f1	snf2_n(HMM:1.3e-17)
4943	nbm700473042.h1.f2	snf2_n(HMM:1.6e-26)
4944	uC-zmflmo17066b08b1.f1	snf2_n(HMM:1.7e-10)
4945	6150_1.R1011.f3	snf2_n(HMM:1.8e-141)
4946	225672_1.R1011.f1	snf2_n(HMM:1.9e-25)
4947	xsy700207459.h1.f1	snf2_n(HMM:2.2e-08)
4948	LIB3076-019-Q1-K1-F10.f3	snf2_n(HMM:2.4e-13)
4949	219582_1.R1011.f3	snf2_n(HMM:2.6e-06)
4950	6423_1.R1011.f2	snf2_n(HMM:2.6e-15)
4951	gct701167820.h1.f1	snf2_n(HMM:2.9e-19)
4952	98888_1.R1011.f3	snf2_n(HMM:3.1e-10)
4953	5603_1.R1011.f3	snf2_n(HMM:3.1e-14),zf-c3hc4(HMM:0.0097)
4954	21514_1.R1011.f2	snf2_n(HMM:3.5e-07)
4955	22960_1.R1011.f1	snf2_n(HMM:3.5e-12)
4956	3233_1.R1011.f2	snf2_n(HMM:3e-23)
4957	LIB3159-002-Q1-K1-E3.f3	snf2_n(HMM:4e-13)
4958	271062_1.R1011.f1	snf2_n(HMM:8.2e-20)
4959	uC-zmflmo17262b09b1.f1	snf2_n(HMM:8.4e-09)
4960	33998_1.R1011.f2	snf2_n(HMM:8.8e-46)
4961	55025_1.R1011.f2	snf2_n(HMM:9.1e-10)
4962	uC-zmflb73275a12b1.f3	srf-tf(HMM:0.00028)
4963	LIB3279-011-P1-K1-D3.f2	srf-tf(HMM:0.00063)
4964	LIB189-006-Q1-E1-G12.f1	srf-tf(HMM:0.0036)
4965	uC-zmflmo17259b12b1.f3	srf-tf(HMM:0.14)
4966	uC-zmflMo17068a10b1.f2	srf-tf(HMM:0.79)
4967	112_4.R1011.f2	srf-tf(HMM:1.1e-35)
4968	LIB3076-018-Q1-K1-A4.f3	srf-tf(HMM:1.2e-17)

4969	uC-zmflmo17039a04b1.f3	srf-tf(HMM:1.4e-29)
4970	LIB3069-009-Q1-K1-H3.f1	srf-tf(HMM:1.5e-33)
4971	CPR9103_L30684201_FL.f3	srf-tf(HMM:1.5e-37)
4972	LIB3069-036-Q1-K1-H9.f1	srf-tf(HMM:1.6e-23)
4973	uC-zmflmo17223f08b1.f1	srf-tf(HMM:1.7)
4974	uC-zmflb73114g10b1.f2	srf-tf(HMM:1.8e-13)
4975	166_2.R1011.f1	srf-tf(HMM:1.9e-29)
4976	uC-zmflmo17001d12b1.f2	srf-tf(HMM:1e-14)
4977	LIB3077-002-Q1-K1-D11.f1	srf-tf(HMM:2.1e-12)
4978	71280_1.R1011.f1	srf-tf(HMM:2.1e-29)
4979	xmt700261644.h1.f3	srf-tf(HMM:2.3)
4980	uwc700151223.h1.f2	srf-tf(HMM:2.5e-09)
4981	LIB3067-028-Q1-K1-H6.f3	srf-tf(HMM:2.6e-23)
4982	166_3.R1011.f2	srf-tf(HMM:2e-30)
4983	111_1.R1011.f3	srf-tf(HMM:2e-35)
4984	LIB3062-002-Q1-K2-B3.f1	srf-tf(HMM:2e-35)
4985	LIB3075-043-Q1-K1-D3.f3	srf-tf(HMM:3.1e-33)
4986	uC-zmflmo17068a10b2.f2	srf-tf(HMM:3.3)
4987	LIB3068-061-Q1-K1-F2.f3	srf-tf(HMM:3.3e-11)
4988	uC-zmflB73003f02b1.f2	srf-tf(HMM:3.6e-06)
4989	g939782.f1	srf-tf(HMM:3.7e-33)
4990	LIB3181-009-P1-K2-C3.f3	srf-tf(HMM:3.9e-36)
4991	611_4.R1011.f1	srf-tf(HMM:3e-36)
4992	uC-zmflb73301e08b2.f1	srf-tf(HMM:3e-36)
4993	122_4.R1011.f3	srf-tf(HMM:3e-37)
4994	uC-zmflmo17184g02b1.f3	srf-tf(HMM:4.2e-10)
4995	543_8.R1011.f3	srf-tf(HMM:4.2e-34)
4996	uC-zmflmo17202h01b1.f2	srf-tf(HMM:4.4e-35)
4997	uC-zmflmo17171b06b1.f2	srf-tf(HMM:4.4e-36)
4998	LIB189-012-Q1-E1-F6.f2	srf-tf(HMM:4.9e-14)
4999	9_1.R1011.f2	srf-tf(HMM:4e-32)
5000	dyk700106944.h1.f3	srf-tf(HMM:5.3e-05)
5001	LIB3079-023-Q1-K1-H5.f1	srf-tf(HMM:5.3e-05)
5002	uC-zmroteosinte058g09b2.f3	srf-tf(HMM:7.2e-16)
5003	g793901.f1	srf-tf(HMM:8.3e-32)
5004	LIB3116-001-Q1-K1-G1.f5	srf-tf(HMM:9.4e-09)
5005	606_1.R1011.f2	tbp(HMM:2.2e-81)
5006	606_2.R1011.f1	tbp(HMM:2.2e-81)
5007	102306_1.R1011.f3	teo(HMM:0.0025)
5008	250289_1.R1011.f1	teo(HMM:0.19)
5009	cat700020547.r1.f3	teo(HMM:0.69)
5010	pmx700086592.h1.f2	teo(HMM:0.88)
5011	LIB3137-013-Q1-K1-A5.f2	teo(HMM:1.1e-27)
5012	135315_1.R1011.f5	teo(HMM:1.6e-08)
5013	LIB84-008-Q1-E1-C5.f2	teo(HMM:2.9)
5014	g5268663.f2	teo(HMM:2e-07)
5015	LIB84-026-Q1-E1-F3.f3	teo(HMM:3e-11)
5016	g2051978.f3	teo(HMM:5.1e-29)
5017	uC-zmflmo17123d12a1.f4	tfiis(HMM:0.00064)
5018	141904_1.R1011.f2	tfiis(HMM:0.00068)
5019	44455_1.R1011.f2	tfiis(HMM:0.087)
5020	g5714238.f6	tfiis(HMM:0.087)
5021	356480_1.R1011.f1	tfiis(HMM:3.5e-19)
5022	2200_1.R1011.f2	tfiis(HMM:3.5e-20)

5023	149396_1.R1011.f1	tfiis(HMM:3e-07)
5024	20390_1.R1011.f2	tfiis(HMM:4e-12)
5025	21886_1.R1011.f1	tfiis(HMM:4e-12)
5026	2200_2.R1011.f1	tfiis(HMM:5.3e-21)
5027	dyk700105135.h1.f2	transcript_fac2(HMM:0.057)
5028	g4804552.f4	transcript_fac2(HMM:2e-17)
5029	10_1.R1011.f2	transcript_fac2(HMM:6e-54)
5030	LIB3150-080-P2-N2-D2.f1	trihelix(HMM:0.061)
5031	35673_1.R1011.f1	trihelix(HMM:1.3e-57)
5032	uC-zmflb73137a02b1.f1	trihelix(HMM:2.5e-06)
5033	xjt700095936.h1.f3	trihelix(HMM:2.6e-10)
5034	10776_1.R1011.f3	trihelix(HMM:2.7e-09)
5035	238186_1.R1011.f1	trihelix(HMM:3.8e-07)
5036	234329_1.R1011.f5	trihelix(HMM:3.9e-18)
5037	80958_1.R1011.f2	trihelix(HMM:5.6e-56)
5038	xjt700095983.h1.f2	trihelix(HMM:7.2e-18)
5039	uC-zmroteosinte105d05b1.f3	wrky(HMM:0.00016)
5040	fwa700097379.h1.f2	wrky(HMM:0.00022)
5041	LIB3069-037-Q1-K1-A10.f4	wrky(HMM:0.0021)
5042	cyk700048751.f1.f3	wrky(HMM:0.0022)
5043	16821_1.R1011.f6	wrky(HMM:0.004)
5044	LIB3069-004-Q1-K1-F1.f3	wrky(HMM:0.005)
5045	uC-zmflb73168d03a1.f3	wrky(HMM:0.0084)
5046	262895_1.R1011.f1	wrky(HMM:0.17)
5047	353348_1.R1011.f3	wrky(HMM:0.17)
5048	85014_1.R1011.f1	wrky(HMM:1.1e-38)
5049	gct701174191.h1.f1	wrky(HMM:1.3e-29)
5050	clt700043633.f1.f3	wrky(HMM:1.4e-12)
5051	14223_1.R1011.f3	wrky(HMM:1.4e-36)
5052	LIB3116-028-P1-K1-A11.f1	wrky(HMM:1.7e-09)
5053	uC-zmflb73017d01b1.f3	wrky(HMM:1.8e-35)
5054	94980_1.R1011.f5	wrky(HMM:1.8e-39)
5055	120742_1.R1011.f3	wrky(HMM:1.9e-33)
5056	clt700041878.f1.f2	wrky(HMM:2.1e-18)
5057	226212_1.R1011.f2	wrky(HMM:2.2e-17)
5058	54216_2.R1011.f3	wrky(HMM:2.2e-29)
5059	wyr700236840.h1.f1	wrky(HMM:2.6)
5060	54216_1.R1011.f1	wrky(HMM:2.6e-25)
5061	LIB84-010-Q1-E1-F10.f2	wrky(HMM:3.2e-21)
5062	uwc700151333.h1.f3	wrky(HMM:3.4e-08)
5063	409_1.R1011.f3	wrky(HMM:3.4e-44)
5064	153602_1.R1011.f2	wrky(HMM:3.6e-18)
5065	23750_1.R1011.f3	wrky(HMM:3.8e-07)
5066	182_1.R1011.f3	wrky(HMM:3e-44)
5067	8386_1.R1011.f3	wrky(HMM:4.2e-37)
5068	153602_3.R1011.f1	wrky(HMM:4e-25)
5069	36570_1.R1011.f1	wrky(HMM:5.3e-07)
5070	68895_1.R1011.f3	wrky(HMM:5.3e-31)
5071	uC-zmroteosinte107d12b2.f1	wrky(HMM:5.8e-17)
5072	151396_1.R1011.f1	wrky(HMM:5e-19)
5073	206462_1.R1011.f2	wrky(HMM:7.1e-38)
5074	24372_2.R1011.f3	wrky(HMM:7.1e-40)
5075	47925_1.R1011.f2	wrky(HMM:7.4e-26)
5076	dyk700106359.h1.f3	wrky(HMM:7.8e-09)

5077	pmx700082065.h1.f2	wrky(HMM:8.4e-05)
5078	uC-zmflb73147h04b1.f3	wrky(HMM:8.8)
5079	xdb700337862.h1.f4	wrky(HMM:9.9e-05)
5080	pmx700089722.h1.f1	wrky(HMM:9.9e-38)
5081	gct701167914.h1.f3	wrky(HMM:9e-15)
5082	g5268376.f3	wrky(HMM:9e-41)
5083	142_1.R1011.f3	zf-b_box(HMM:0.00024),zf-constans(HMM:4.3e-32)
5084	142_2.R1011.f2	zf-b_box(HMM:0.00024),zf-constans(HMM:4.3e-32)
5085	68636_2.R1011.f3	zf-b_box(HMM:0.0075),zf-constans(HMM:3.7e-38)
5086	61495_1.R1011.f2	zf-b_box(HMM:0.063),zf-constans(HMM:3.9e-15)
5087	8146_2.R1011.f3	zf-b_box(HMM:0.088),zf-constans(HMM:3.9e-39)
5088	157403_1.R1011.f4	zf-c2h2(HMM:0.00021)
5089	wyr700240638.h1.f2	zf-c2h2(HMM:0.00024)
5090	53008_1.R1011.f1	zf-c2h2(HMM:0.00025)
5091	419_1.R1011.f3	zf-c2h2(HMM:0.00056)
5092	LIB3115-015-P1-K1-F5.f1	zf-c2h2(HMM:0.0008)
5093	41347_1.R1011.f3	zf-c2h2(HMM:0.00091)
5094	209161_1.R1011.f3	zf-c2h2(HMM:0.00099)
5095	LIB3069-042-Q1-K1-H12.f2	zf-c2h2(HMM:0.0014)
5096	fdz701160730.h1.f1	zf-c2h2(HMM:0.0022)
5097	57582_1.R1011.f1	zf-c2h2(HMM:0.0024)
5098	fC-zmst700894694a1.f1	zf-c2h2(HMM:0.0027)
5099	uC-zmflb73027h12b1.f1	zf-c2h2(HMM:0.0029)
5100	LIB3088-019-Q1-K1-F8.f3	zf-c2h2(HMM:0.017)
5101	LIB3136-023-Q1-K1-C2.f2	zf-c2h2(HMM:0.017)
5102	LIB3151-023-Q1-K1-G2.f2	zf-c2h2(HMM:0.022)
5103	157260_1.R1011.f1	zf-c2h2(HMM:0.033)
5104	uC-zmflb73260g05b2.f3	zf-c2h2(HMM:0.043)
5105	347503_1.R1011.f1	zf-c2h2(HMM:0.071)
5106	pwr700453237.h1.f4	zf-c2h2(HMM:0.087)
5107	14895_1.R1011.f2	zf-c2h2(HMM:0.1)
5108	16240_1.R1011.f2	zf-c2h2(HMM:1.3e-05)
5109	191_1.R1011.f1	zf-c2h2(HMM:1.6e-15)
5110	g4966708.f4	zf-c2h2(HMM:1.8e-10)
5111	xyt700346018.h1.f3	zf-c2h2(HMM:1.9e-25)
5112	411_1.R1011.f2	zf-c2h2(HMM:2.2e-07)
5113	uer700582866.h1.f2	zf-c2h2(HMM:2.4e-06)
5114	LIB3068-001-Q1-K1-C7.f2	zf-c2h2(HMM:3.2e-34)
5115	1085_1.R1011.f1	zf-c2h2(HMM:3.4e-28)
5116	415_1.R1011.f1	zf-c2h2(HMM:3.6e-09)
5117	yyf700352188.h1.f2	zf-c2h2(HMM:3.6e-21)
5118	uC-zmflmo17070f07b1.f3	zf-c2h2(HMM:4e-06)
5119	419_3.R1011.f2	zf-c2h2(HMM:6.8e-09)
5120	262434_1.R1011.f2	zf-c2h2(HMM:6.9e-10)
5121	312453_1.R1011.f1	zf-c2h2(HMM:7.1e-06)
5122	g3170600.f1	zf-c2h2(HMM:7.7e-09)
5123	nwy700447294.h1.f2	zf-c2h2(HMM:8.4e-19)
5124	LIB189-028-Q1-E1-F5.f1	zf-c2h2(HMM:9.7e-07)
5125	159463_1.R1011.f6	zf-c3hc4(HMM:0.00013)